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PARADEMARKS.	

11	31	51 186	71 246	91 306	111 366	131 426	151 486	171546
CIC	G GGA	L	L CTG	G GGA	$^{\mathrm{C}}$	P CCA	S AGT	ე 10
L CTG C	P	A GCA	T ACT	D GAT	$^{ m Y}$	N AAC	I ATC	F
A GCC C	9 9	T ACA	N AAC	P CCA	K AAG	G GGA	C TGC	C TGC
L CTC G	L	W TGG	$^{ m Y}$	N AAT	W TGG	H CAT	TACT	A GCT
R CGC C'	295 GGC	N AAC	P CCA	R AGA	Y TAC	D GAT	Q CAA	Y TAT
A GCC C	P	Q CAG	H CAT	ပ Hgc	V GTC	K AAG	I ATA	9 9
A GCC G	S AGC	TACA	Q CAG	Y TAT	GGT	$^{ m Y}$	T ACC	s TCA
L GC	P CCT	G GGA	F	N AAC	D GAT	C TGC	CIC	E GAG
P CCG C(A GCG	R AGG	TACT	H CAC	E GAG	9 9	K AAA	M ATG
A GCG C	P	Y TAT	EGAG	E GAG	H CAC	L	N AAC	G GGG
M ATG G	R CGG	D GAT	N AAC	G GGT	E GAG	N AAC	S	A GCT
CC A	A GCC	A GCG	W	L CTG	A GCA	G GGA	T ACG	F TTT
CGGC	A GCG	G GGT	FTTT) 9	V GTG	PCCT	K AAA	K AAG
CGTC	L	N AAT	$_{ m L}$	999	Y TAT	M ATG	S AGT	$_{ m F}$
CACG	T ACG	A GCC	C TGT	E GAG	C TGC	Q CAG	TACC	R AGG
CGCC	L	T ACA	P CCA	999	W TGG	C TGC	9	Q CAG
CĠTC	. A GCG	F TTC	K AAG	N AAC	CCC	A GCT	T ACT	S AGT
CACG	A GCG	C TGT	G GGG	P	S AGC	P CCT	L CIA	R CGG
GTCGACCCACGCGTCCGCCCCC	A GCC	E GAG	GGC	Y TAC	V GTG	I ATA	P CCT	C TGT
GTC	S TCC	PCCC	Q CAA	K AAA	D GAC	E GAG	P CCT	${ m F}$

Fig. 1A

2/95 $\frac{191}{606}$ 211 666 231 726 251 786 271 846 291 906 311 966 1026 331 V GTC TACT D GAC A GCC E GAG PCCT N AAT R AGG S AGC D GAT PCCT G GGG VGTG PCCA I ATC E GAG N AAC S TCC F TTT P M ATG R CGC R GGC Q CAG C TGC Y TAT L VGTT D GAC S AGC D GÀT P CCA E GAA IATC V GTC A GCG R CGG R AGG $_{
m L}$ S TCT T ACC V GTG I ATC I ATC S TCG GGG $_{
m F}$ E GAA S AGT R AGG S TCT TACC D. GAC H CAC $^{\rm F}$ E GAA A GCC 9 96C \overline{W} S TCT R AGG $^{\mathrm{F}}$ Y TAT K AAG A GCA D GAT M ÄTG Y TAC I ATC R CGC $_{
m L}$ V GTC E GAG 9 9 A GCC C D GAC I ATC A GCC A GCC G GGG V GTC GGT S TCA FTT L CTA V GTC CAA $^{
m Y}$ $_{\rm TGT}^{\rm C}$ $^{
m Y}$ R AGG L CTA V GTC \mathbf{F} TTC $^{
m Y}$ K AAG N AAC P G GGG PCCC R CGT D GAC L TTA W TGG G GGG T ACG $_{
m L}$ Q CAA F TTC H CAC V GTT Y TAC T ACC A GCC GGT S AGC T ACC S TCT A GCT D GAT H CAC C TGC ${
m Y}$ TAT Y TAC V GTC F TTC F TTT PCCT DGAT A GCC TACC H CAC 9 N AAC G GGA N AAT GGG 9 D GAC I ATC $^{\mathrm{F}}$ Q CAG D GAT N AAC F TTC V GTG P H CAC L CTG s TCC A GCC

 $^{\rm C}$

L CTC FTTC

S TCC LCIT

 $_{
m L}$

Q CAG

G GGA

Fig. 1B



351 1086 371 1146 S AGC Q CAG V GTC PCCT S AGT P CCA CIC CAC N AAC S AGC A GCC P Q CAG S AGC E GAG TACC T ACG T ACC I ATC I ATC V GTG V GTC E GAG Y TAT A GCC LCTC VGTG V GTC T ACG K AAA Q CAG S TCC N AAC S V GTC R CGG A GCT A GCC P A GCT

391 1206 E GAA VGTT R AGA H CAC S AGC GGA A GCT G GGG M ATG PCCC P CCA A GCG W TGG S TCC N AAT S AGC GGT P CCA V GTC T ACT

411 1266 A GCA V GTA I ATT A GCC T ACA V GTC T ACA L I ATC LCTC LCIC T ACT A GCA Γ GGT Y TAT V GTC T ACA \overline{W} GGA

431 1326 R AGG LCIT D GAC GGG S TCA A GCT PCCT VGTT R CGT H CAT S TCC K AAA $_{
m TTC}$ TACA V GTC H L CTG LCTT I ATA K AAG

451 1386 TACT S TCC PCCT K AAG YTAC F TTT I ATT S AGC W TGG I ATC E GAA G GGG S TCG TACT G GGG P CCA Q CAA H CAT $_{\rm TGT}^{\rm C}$ D GAT

471 1446 PCCC AAT z R. CGC D GÀC D GAT Q CAA Q. CAA S AGT Q CAG GGT K AAG L CTC K AAA K AAG K AAG F TTT I ATC S TCC I ATT S TCA

L V S D * CTT GTG AGT GAC TAA

476

Fig. 1C

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1657 AAACCCCACTGTGCCTAGGACTTGAGGTCCCTCTTTGAGCTCAAGGCTGCCGTGGTCAACCTCTCCTGTGGTTCTTCTC 1540 TGACAGACTCTTCCCTCTCTCCTCTGCCTCGGCCTCTTCGGGGAAACCCTCCTACTACAGACTAGGAAGAGGCCACCT 1620 GCTGCCAGGCAGGCAGAGCCTGGATTCCTCCTGCTT

Fig. 1D

79	19 137	39	59 257	79	99
2255	A GCG	D GAT	N AAC	295 9	E GAG
rgac(L l	A GCA	W TGG	L CTG	A GCC
3CAC!	T]	GGT	F	G GGA	V GTG
rccc	L CTC A	NAAC	L	G GGA	YTAC
3GGG	A]	A GCC	C TGT	E GAA	C
CCG		T ACA	P CCA	999	\overline{W}
BCGC	A A	$_{ m TTC}$	K AAG	N AAC	P CCT
36600	s A	C TGC	9 9	CCC	S AGC
מכככ	L S CTC TCC	E GAG	G GGT	Y TAC	V GTG
rctg	L I CTG CI	PCCC	Q CAA	K AAG	D GAC
ממכנו	A I GCG CI	9 9	L	L	G GGA
TGC		S TCC	A GCG	T ACG	D GAT
3GTĞ(t T	R CGC	T ACA	N AAC	P CCA
וכככנ	A R GCC CGT	P	W TGG	YTAC	N AAT
3GGC1	A A GCC GC	G GGT	S AGC	P	R AGA
36000	P A	P	Q CAG	H CAT	C TGC
GTCC	_	A GCG	T ACA	Q CAG	Y TAT
ACGC	L P	P CCC	G GGA	F	N AAT
GTCGACCCACGCGTCCGCCCCGGTTGCTGCCCCCTCTGCCCCGGGCCGCC	I A	R CGG	R AGG	T ACT	H CAC
GICG	M C ATG	A GCC	$_{ m TAC}^{ m Y}$	E GAG	E GAG

Fig.1E

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139 497 159 557 199 677 179 617 219 737 239 N AAC S TCT A GCT G GGG GGT S TCA V GTC F TTT $_{
m L}$ GGA T ACC F TTT H CAC C TGC $^{
m Y}$ R AGA Γ V GTC K AAA PCCT K AAG K AAG PCCC N AAC GGC TACC R M ATG S AGT W TGG F TTC Q CAG GGG T ACT F H CAC Q CAG TACC $^{
m Y}$ R AGA T ACG G GGT A GCC N AAC TACC D GAC C TGC G GGC Q CAG H CAC C TGC Y TAC Y TAC $_{
m F}$ A GCC T ACG S AGT PCCT D GAC A GCC T ACC H CAT G GGC PCCT L R CGG N AAT D GAC GGG GGC IATC D GAC C TGT N AAC PCCT \mathbf{F} V GTG PCCT R CGC Γ . 9999 E GAA PCCT F TTC C TGC LCIC F TTC L CTG S TCT $^{\rm C}$ S AGC $^{
m C}_{
m TGT}$ P CCA V GTC TACT E GAG D GAC A GCC Y TAC N AAC I ATC $_{
m TTC}$ S AGT D GAC PCCT G GGA VGTG K AAG GGA $^{\rm C}$ $^{\rm C}$ N AAT F TTT S TCC M ATG P CCA W TGG T ACC A GCC H CAT C TGC L $^{
m Y}$ V GTT D GAC Y TAC Y TAT D GAT Q CAA E GAG V GTG I ATC R CGG A GCA V GTC K AAG I ATA 9 66C TACC I ATT V GTG I ATC S TCT GGA Y TAC T ACC S TCA S AGC R AGG A GCC TACC D GAC D GAC C TGC LCTC E GAG A GCC R AGG - ဗ A GCA W TGG E GAG M ATG GGC K AAG A GCG D GAC I ATC M ATG Y TAC H CAT LCTT N AAC G GGG E GAG 999 9 A GCC C TGC D GAT

Fig.1F

6/95

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TRADEMART 339 359 1157 379 319 399 459 1277 419 439 1337 V GTC Q CAA VGTG V GTC R CGT S TCC L I ATA AGG 24 Y TAC F TTT E GAG Y TAT H CAC P N AAT E GAG S TCA D GAT $_{
m L}$ A GCA LCIC G GGG L TTA R CGA $_{
m CTG}$ S AGC Γ V GTG L CTG V GTC PCCT WTGG R AGA H CAT L S A GCT T ACC K AAA I ATT A GCC s TCA GGG R AGA V GTC Q CAG A GCC F TTT S TCC T ACG M ATG Γ $_{
m L}$ N AAT GGA N AAC S V GTA $^{\mathrm{C}}$ C TGC S AGC S TCT F TTC Q CAG V GTC H CAC Q CAG $_{
m L}$ \mathbf{F} TTC V GTC P CCA S TCT A GCC A GCT A GCC G GGA A GCC $^{
m F}$ V GTC S TCT L Q CAG PCCT A GCT TACT D GAT r AGA T ACT o Caa R AGA PCCT N AAT S AGC Q CAG K AAG G GGG O CAA L CTA P CCG I ATC E GAG V GTC P CCG WTGG s TCG $_{
m LTA}$ P CCA R CGC Q CAG E GAG $_{
m L}$ R CGC S AGT PCCT T ACC LCIT S AGC P CCA L CTC Q CAG D GAT H CAC T ACA E GAG N AAC R AGG P CCG S TCT N AAC S AGC A GCC Q CAG M ATG Q CAG GGG FTTC E GAA A GCC P T ACA s TCA H CAT S TCT E GAG S AGT $^{
m F}$ Q CAA S AGC Q CAG P CCA $_{
m CTG}$ F TTT LCTC K AAG ${
m Y}$ TAT E GAG P GGG s TCA s TCC P CCA R CGG $_{
m L}$ TACC TACC T ACC $_{
m L}$ S TCC E GAG GGA V GTC I ATC I ATT A GCC I ATC Q CAG s TCA I ATC S TCT



STC AGA GTC AAC AAG ATG ACC GCA ATC CCC TCG

1572 2046 2599 1809 1888 2283 2362 2836 1967 2678 2441 2915 2994 STGACTGAAGCCCACGCCTGCATGAGAGGCTCCGCTCCAAGCTCGAGTTTGCTCCCCTGAGTTCTCCTCTGATGAGTTC CCTGCCTTCCCATTCACCACCATCTCTTTTGGGAGCACCCTGCTTTAGAGGCAGCCCAGCCTGGGATCCTCCATCACAT STACCAGCCTGCTCTCTGCTGGGGATGGTAAGACAGGCCCCAGGCTGACAGGACACAGCTGGACCTGACTCCAGAAGA CTCTTGGGTGGTGGGGGGGTATAGTGTAGGATGAGTTTTCTTGCTTCTTCTTCTTGTTTTGTCCACATACAGATCGGTTTTC CCCTGTCTTTACAGTTTGCAATAGAGCCAGACTGAAAGAACTGTCAGGTTTTCTAGGCTGGCCTGGTTCCCCCACTAAGA AGTCCGAGGGGACTGAGAGCAGGGCCACACACAGATGTCATCTTTCTAGAGGGTTCTTTTAGTACCCACTGACCAATGG STGGCATTGGCGCCCCTAGAGGCCCCAGAGGCCCAGTGTAGGCTTGGAGCTTTCTCTGCTGCCAACTACCATGTGTCATCT PAGCCCTCAAGTAGTTGCCAATCCTGTGGAATCAGAATTCAGCCTGTCTTCCTGTCCTCAGCCCAAGCCTGTAGCCTAG TGGGGCTGTAGCACAGAGCTGGGGCTGTAGCCTAGAGCTGGGGCTGTAGCACAGAGCTGGGGGCTGTAGCACAGAGCTGG AGCTGGGGCTGTAGCCTAGAGCTGGGGCTGTAGCCTAGAGCTGGGGCTGTAGCACAGAGCTGGGGGCTGTAGCCTAGAGC ITCCTACGTGAGGTGTCATCATTTTAAAAGCAGATCAAAACTACCGCGAGTTTTGTCCTTTGTCCCTTATCATGGGAGC <u> AGAGTAGGAGTAAGGGCTCTGGTCTTGCTCATTGTCCCCCAGACAGGGAGGCAGGAAAAGGTCAGGCTTGGGAACTGGA</u> SATCCTCCCAGGAAAAGCTGCAAGATTGAGAGCCCCAGCTGCAGTTGGGAGGAGGAAGGGCCATCCCCGACTGAGAAGTC PACAGGGGTACTAAGCTAGGGGGTCATCTCATTTGATCTGGGAAAGGCTACAGGCTCCTGGATGTGAAGACAGGCC CTGCAGTCTGGAAGTGGCCTTTGTCAGCAGCAGCTGTGCCCTGAAGGTAGACCTTGGTCACTCTCCTGCCAGCCCTTGA CACTACATAAGAAGACCACTGGAAATAGACTGACAGGAGCAGGTTCCACTCTAGGCTGTCCATAGCGTTTGCAGGACTC

Fig.1H

8/95 3547 3626 3784 3863 4100 3942 4258 4337 4495 4653 4890 CCCTGAGACCAAGTGTTGAGTCACAGAGTGCCATGTGCGTAGTGCATAAAGGATATGGGTTCTTAACCAGGGAAGGCTC ATCTCGGACACAGGAAGCAAGCCCCCAGTGTGGTGGCAGCTGCGGCTCAGCATTGGTGTCCCCCAGGAAGGGCGGTGGATG TGCCCACGCTCCTTTTGCTGTGGGCCTGGCCACACCCAACACTGCAGGGCCCACCTTCTCTTTTGGGGGGTAGGGACAC ATAGCAGGCCAGGACATTTTTCAGCTCAGAGCACTGGCCCCAGGCTTCCTCTAAGCCACCACTCAGCTGTCTTCTTCCT AAAGCTCTTGAAGATCAAAGCTCTGGCGGGTACAGCTGTCCTGGCCTGTGGGCCAGCCCATGGGATGTGCCTGGGCCAG GAGCTCGCGCCGGCTGTTGCCAGGGACAGACTGACTACACTTGACCTTCAAGAGCACTTAGAAGTGGATGGCCTCCAGA TCCTGTCACACTGCTTACAAAGCAGAGACAGAGTAGGAAAGAGGTCTTCATCCTCTCCCACATCAGCAAGGATAGGGCT GCGGCTGCCTAAAGTGAGCAAGGAGAACAGAGCTCTGGACTTCTCTAAATGTGGGGCTCTGGCTTCAGACTCCTCAGCCA CTCTGTCAGCCTCTGCAGGGGCCACACACACTCTCCCGAGCCAAGTCCACAAGCCTCCATGGTTCCCTGGCTCCTCTCCT GTGGAGTGTCCTGTTTGATGTCTGAGGTCTGCTTTGGGTACCGCCCTGGGAACTGCTAACCTCCGATTGGTCCCTTTGT GGCTGCACCCCCACCCTGGTCTGCCAACAGAACCTGGGGGCCTCACACGGGCTCCTGTCTTGCCAAGCTGGAGCTGAGC AGATCCAGCGAGGGAGCTGCCATCCCGGCCACCTTCATAGCAGCAAGACCTTCCCATTTCCAATCTCACCTCCAGCAG GGATATGACTTTGGACAACAAGGCTTTATTTGTAAATATGCTCTTAATATGCAACTTTGAGAATAAGATAGAAACATCA TTGTTGTAGAAAAAAAAAAAAAAAAAAGGGCGGCCGC

Fig. 1

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10 20 30 40 50 60 70 Hum. MAPPAARLALLSAAALTLAARPAPSPGLGPGPECFTANGADYRGTQNWTALQGGKPCLFWNETFQHPYNT ::::::::::::::::::::::::::::::::::::	80 100 110 120 130 140 LKYPNGEGGLGEHNYCRNPDGDVSPWCYVAEHEDGVYWKYCEIPACQMPGNLGCYKDHGNPPPLTGTSKT :::::::::::::::::::::::::::::::::::	150 160 170 180 190 200 210 SNKLTIQTCISFCRSQRFKFAGMESGYACFCGNNPDYWKYGEAASTECNSVCFGDHTQPCGGDGRIILFD ::::::::::::::::::::::::::::::::::::	220 230 240 250 260 270 280 TLVGACGGNYSAMSSVVYSPDFPDTYATGRVCYWTIRVPGASHIHFSFPLFDIRDSADMVELLDGYTHRV ::::::::::::::::::::::::::::::::::::
Hum. MAPPAA ::::: Mur. MAPPAA	Hum. LKYPNG :::::: Mur. LKYPNG	Hum. SNKLTI :::::: Mur. SNKLTI 140	Hum. TLVGAC :::::: Mur. TLVGAC 210

Fig.1.

MAR 1 5 2004 ES
ADEM

	290	300	310	320	330	340	350
Hum.	Hum. LARFHGRSRPPLSFNVSLDFVILYFFSDRINQAQGFAVLYQAVKEELPQERPAVNQTVAEVITEQANLSV	FNVSLDFVILY	FFSDRINQAQ	3FAVLYQAVK	EELPQERPA	VNQTVAEVITEQ	ANLSV
Mur.	Mur. LVRLSGRSRPPLSFNVSLDFVILYFFSDRINQAQGFAVLYQATKEEPPOERPAVNOTLAEVITEOANLSV	FNVSLDFVILY	FFSDRINGAQO	SFAVLYQATK	EEPPOERPA	::::::::::::::::::::::::::::::::::::::	SSSS ANT.SV
	280 290	300	310	320	330	340	,
	360	370	380	390	400	410	420
Hum.	Hum. SAARSSKVLYVITTSPSHPPQTVPGSNSWAPPMGAGSHRVEGWTVYGLATLLILTVTAIVAKILLHVTFK	TSPSHPPQTVP	GSNSWAPPMG?	AGSHRVEGWT	VYGLATLLI	LTVTAIVAKILL	HVTFK
	•••••••••••••	•	:			•	•
Mur.	Mur. SAAHSSKVLYVITPSPSHPPQTAQVAIPGHRQLGPTATEWKD-GLCTAWRPSSSSQSQQLSORFFCM	PSPSHPPQTAQ	VAIPGHRQLG	PTATEWK	D-GLCTAWR	PSSSSSSOCISO	RFFCM
	350 360	370	380	390	0	400 410	0
	430	440	450	460	470		
Hum.	Hum. SHRVPASGDLRDCHQPGTSGEIWSIFYKPSTSISIFKKKLKGQSQ-QDDRNPLVSD	HOPGISGEIWS	I FYKPSTSIS1	FKKKLKGQS	Q-QDDRNPL	VSD	
		•	•	••	:	•	
Mur.	SHINLIESLHQETLGTVVSLGLLEISGPFSMNLPLQSPSLRRSSRVRVNKMTAIPS	LGTVVSLGLLE	ISGPFSMNLPI	QSPSLRRSS	RVRVNKMTA	IPS	
	420	430 4	440 45	450 460	09	470	



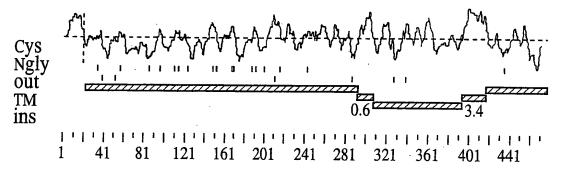


Fig. 1L

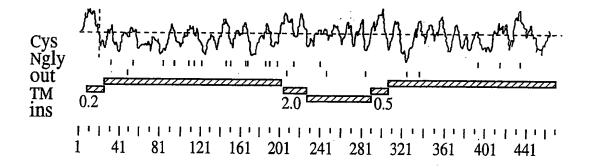


Fig. 1M

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7			-	121,00		•	
13	33 126	53 186	73	93	113 366	133 426	153 486
GGA	N AAT	GGA	C TGT	FTT	D GAT	G GGA	$_{ m CTG}$
F TTT	L CTG	N AAT	V GTG	P CCA	L	W TGG	N AAT
D GAT	L	V GTC	T ACT	C TGT	W	E GAA	A GCC
I ATT	L	$_{ m CTG}$		G GGA	I ATT	R CGG	E GAA
H CAT	I ATC	R AGG	W TGG	L	K AAA	H CAC	GGT
WTGG	C TGC	$_{ m L}$	Q CAG	Q CAG	G	Q CAA	Y TAT
S	T ACT	E GAG	GGA	K AAA	H CAT	C TGT	C TGT
N AAC	V GTA	Γ	Q CAG	C TGC	R AGA	E GAA	N AAC
Q CAA	V GTG	D GAT	F TTC	V GTG	T ACT	W TGG	V GTG
P	A GCT	T ACA	K AAA	V GTC	V GTG	CIC	GGT
L	S TCT	G GGA	V GTG	T ACT	A GCC	A GCT	V GTT
M ATG	F	N AAT	E GAG	S TCA	Q CAA	S TCA	D GAT
M ATG	L	F	V GTG	A GCC	G GGA	E GAG	E GAA
AGTA	N AAC	S AGT	T ACA	T ACT	F TTT	N AAT	G GGA
AACT	Q CAG	S AGC	999	T ACT	R CGT	G GGA	H CAT
CTAG	H CAT	I ATC	S TCT	N AAC	F TTT	Y TAT	Y TAT
3GAT(C	L	C TGC	W TGG	M AŢG	C TGT	C TGT
CTCG	C TGC	T T T	P CCC	9	A GCC	S TCC	N AAC
GCGGCCGCTCGCGATCTAGAACTAGTA	C TGC	C TGC	G GGT	D GAT	F	V GTT	H CAT
ງອວອ	R AGA	S TCC	D GAC	D GAT	S TCT	D GAT	S AGC

Fig. 2A



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173	193 606	213	233 726	253 786	273	293 906	313	333 1026
Q CAA	C TGC	V GTA	N AAT	T ACT	GGG	N AAT	9	G GGT
FTC	V GTG	A GCT	W TGG	L TTA	M ATG	N AAC	A GCT	S TCC
K AAA	V GTG	P CCT	L	T ACA	$^{ m C}$	W TGG	F	$^{\mathrm{C}}$
V GTG	A GCC	S AGC	A GCA	V GTC	CGC CGC	K ÄAG	H CAC	S TCC
E GAG	A GCT	N AAT	$_{ m L}$	D GAT	N AAC	H CAT	$_{ m CTT}$	V GTC
V GTG	T ACT	V GTT	E GAG	E GAG	T ACT	H CAC	A GCA	GGT
R AGA	N AAT	V GTT	N AAT	N AAT	G GGA	C TGC	T ACC	D GAT
G GGG	$_{ m L}$	GGA	999	H	G GGT	V GTA	G	L
S TCA	N AAC	S TCT	Q CAG	S AGT	V GTA	TACC	C TGT	WTGG
C	W TGG	S TCT	C	C TGC	L	999	G GGA	V GTA
S	999	I ATT	L TTA	D GAC	R AGG	W TGG	L	V GTT
N AAC	D GAT	T T T T	I ATT	H CAT	L CTA	R AGG	Q CAG	D GAT
N AAC	D GAT	S TCT	D GAC	N AAT	E GAA	GGA	K AAG	S TCT
G GGA	C TGT	S TCT	D GAT	GGA	L	Q CAA	C TGC	GGG
D GAT	I ATA	P CCA	L	W TGG	D GAT	IATC	V GTA	S TCA
V GTG	TACT	C TGT	W TGG	G GGA	S AGT	K AAA	V GTC	Q CAG
L CTA	999	G GGA	I ATT	R CGT	S AGT	$_{ m CTG}$	D GAT	$_{ m L}$
R AGG	W TGG	L CTA	PCCC	H CAT	D GAT	E GAG	A GCT	H CAT
$rac{ ext{L}}{ ext{TTG}}$. R AGG	Q CAA	R CGC	R AGA	Y TAT	V GTA	A GCA	P
GGT	E	R AGG	$_{ m L}$	C TGC	$^{ m C}$	R AGA	A GCT	$_{ m L}$

Fig. 21

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PROPERTY OF TRADEMENT OF THE PROPERTY OF THE PRO

H CAT L CTT $^{\rm C}_{
m TGT}$ D GAC F TTT N AAT V GTC TACC G GGA S TCC H CAT R AGA $^{\rm C}$ D GAC W TGG L CTT F TTT S TCT E GAA N AAT 373 1146 D GAT A GCA L CTA R CGA L CTG E GAA $\frac{1}{1}$ D GAT A GCA GGA D GAT S TCA C TGC I ATC V GTG S TCT V GTG D GAT N AAC Q CAA

393 1206 I ATA T ACA W TGG W TGG Q CAG E GAA H CAT I ATT R AGA VGTG E GAG V GTA R AGA G GGG S TCA $^{\mathrm{C}}$ N AAT N AAC S AGT

> G GGA

413 P $^{\mathrm{C}}$ G GGA L CTA Q CAG K AAG $_{\rm TGT}^{\rm C}$ VGTT VGTG L A GCC Q CAA E GAA N AAT K AAG \overline{W} . N AAC Q CAG D GAC $^{\mathrm{C}}$

433 1326 I ATA W TGG I ATT D GAC R AGA A GCT E GAA N AAT S AGT PCCT K AAA A GCT R CGT R CGT S AGT 9 660 F TTT V GTC S AGC \mathbb{F} TTC

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1386 453 K AAA GGA D GAT Y TAT T ACA C TGC D GAC W TGG L CTC A GCT S TCA E GAG N AAT G GGG TACT CS TCT I ATA S AGC N AAC

473 1446 D GAT A GCA K AAG D GAT s TCT $^{\rm C}$ I ATT V GTA GGA A GCT D GAT S TCA R AGA R CGA F TTC C TGC T ACA R CGA K AAG A GCA

493 $^{
m Y}$ K AAA GTG E GAG $_{
m L}$ R AGA G GGG Y TAT $_{\mathrm{TGT}}^{\mathrm{C}}$ P S AGC H CAT À GCT G GGG V GTC L R AGG L CTA D GAC $_{
m L}$

513566 A GCT A GCA N AAT R AGG T ACA SAGC W TGG R AGA D GAC H CAT CTGT V GTG TACT G GGG W TGG E GAG G GGA O CAA

Fig. 2C

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TRADEMARK OF TRADEMARK 553 1686 1866 573 1746 593 1806 1926 613 633 653 986 673 2046 693 2106 GAA W TGG V GTA S TCG N AAC M ATG D GAT S AGT GTG > K AAA I ATC I ATT C TGC W TGG 9 9 9 9 $_{\rm TGT}^{\rm C}$ C TGC LCTT F TTT V GTG N AAT R I ATT GGC S TCC D GAC R AGG D GAT S TCA Y TAT N AAC D GAC I ATC V ĞTT N AAT L CTG TACC E GAG E GAG S AGC D GAT S TCT D GAT N AAT E GAG M ATG N AAT R AGA 9 9 $^{\rm C}$ S TCT D GAT M ATG GGA GGT GGA H CAC 9 9 V GTG P CCA L W TGG D GAT F TTT I ATT V GTA V GTG T ACA $^{\rm C}$ \overline{W} TGG G GGG s TCG V GTG C $^{\mathrm{C}}$ $_{
m L}$. 9 D GAC I ATT S AGT A GCA N AAT H CAT S TCT R AGG W TGG $_{\rm L}$ K AAA N AAC D GAT M ATG H CAT Γ R CGG V GTT R AGG Q CAG G GGA s TCT D GAC K AAG 9 9 GGA S AGC Y TAT C TGC CTGT s TCA K AAG D GAT GGA WTGG Q CAA $_{\rm TGT}^{\rm C}$ GGA I ATC G GGA T ACA Γ WTGG \mathbf{F} TTT VGTG T ACA W TGG V GTG $^{\rm C}$ W TGG GGA A GCA $^{
m Y}$ VGTG S TCT L GGA D GAT A GCT S AGT VGTG D GAT A GCT V GTT Ç $_{
m ITG}$ P CCT H CAC GGT E GAG A GCA N AAC s TCA D GAT E GAA o Caa GGA S TCA $_{
m CTG}$ G GGA E GAG E GAA A GCT G K AAA TCA $^{\mathrm{C}}$ $^{\rm C}$ R AGA K AAA $_{
m L}$ D GAT S AGT വ D GAC T ACC GGA H CAC S AGT GGT GGA

16/95

TRADEMARK OF TRADEMARK 733 713 I ATT CTGT GGA E GAA L GTG A GCC Q CAA R AGG GGT Q CAG C TGC V GTC V GTT N AAT V GTT V GTG E GAA E GAG A GCT V GTT I ATT K AAA N AAC M ATG G GGA GGA W TGG R AGG 9 9 S AGC N AAT S AGC A GCT

CTGT

L CTG

GGT

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753 2286 $_{
m L}$ I ATC H CAC L TTA T ACA R AGA E GAA TACA \mathbb{F} TTC H CAT PCCT E GAG R AGA S TCC V GTC R AGG I ATC A GCA S TCT G GGG

773 E GAG WTGG R CGA I ATA $_{\rm TGT}^{\rm C}$ D GAT \overline{W} LCIC S TCT A. GCC E GAA G GGG GGA TACT $^{\rm C}$ 9 96C S TCT N AAT S TCG M ATG

793 R AGG H CAC A GCC S TCA $^{\rm C}$ I ATC $_{
m ITG}$ S AGT A GCA E GAA M ATG N AAT $_{
m L}$ H CAT $^{\rm C}$ A GCG TACT Q CAG K AAA W TGG

813 2466 A GCA H CAT K AAA V GTG E GAA VGTT R CGT GGA S TCT သ TGC PCCC M ATG D GAT A GCT G GGA V GTT Γ R AGG PCCC Q CAG

833 2526 $^{\rm C}$ $_{
m L}$ V GTG N AAT A GCC A GCT H CAT LCTT S TCT $_{
m F}$ D GAT S TCT D GAT $^{\rm C}$ V GTC S TCT CGC W TGG T ACA D GAC

853 2586 G GGG K AAA GGA F TTT H CAC D GAT G GGA V GTG S TCT LCTT S TCT I ATA A GCC D GAT G GGA $^{\rm C}$ N AAT $_{
m TTA}$ E GAÀ R AGA

873 2646 L TTA A GCA LCTT H CAC TACT E GAA S AGT . GGG E GAA $^{\rm C}$ Q CAG FTTC K AAG E A GCC W TGG T ACT L CTA G GGT N AAT

2E Fig.

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913 2706 933 953 2886 893 973 2946 3008 1013 3066 1033 3126 993 1053 V GTC V GTG E GAG D GAT K AAA N AAT N AAT GAC Ω V GTT Q CAA E GAA GGA N AAT GGA E GAG A GCA \succ G GGG G GGA G GGG P CCA GGA H CAT LCIC I ATC L TTA V GTT D GAC D GAC T ACA L TTA I ATC C TGC C TGC 团 E GAA W TGG TACC CTGT C TGC $^{\rm C}_{
m TGT}$ PCCA I ATC V GTA R AGA Q CAG H CAC S TCA H CAŢ PCCC F TTT $_{
m ITG}$ R AGA A GCT S AGC S TCC TACC LCTC $_{
m L}$ PCCT F TTT G H CAC R AGG K AAA D GAC A GCA A GCT P CCA S AGT A GCC G GGA I ATC 9 96C CTGT TACT H Q CAG 9 9 9 9 $_{\rm TGT}^{\rm C}$ C TGT L CTG N AAT . GGG E GAG G GGA LCTT T ACC α T ACT V GTG S TCA WTGG Γ $^{\rm C}_{
m TGT}$ PCCA S AGC V GTT D GAC L CTT S AGC V GTG TACA S AGC D GAC 9 96C V GTT E GAA \overline{W} M ATG R CGA L CTC R CGT G GGA A GCA Ŋ P Q CAG V GTC H CAC V GTT Q CAA T ACA s TCT D GAT H CAT D GAT G GGA R AGA C TGC L TTG S AGT $^{\rm C}$ > CAA T ACA L CTA C TGC R AGA N AAC I ATC L CTT Y TAT Y TAT VGTG V GTG V GTT L CTA E GAA D GAT P CCA R CGC I ATT N AAC L CTG DGAC L R CGA GGA S TCT V GTT PCCC S TCC I ATC R CGT I ATT L CTT V GTC S TCT R CGG E GAG A GCC S TCA T ACT V GTA K AAA CTGT Y TAT

2F Fig.

CAC

TAT

GAG

GGG

CGC

GGG

GTG



1093 3306 1113 1133 3426 3486 1193 3606 1213 3666 V GTG E GAG \overline{W} V GTC A GCT TACC S AGC PCCT S AGC VGTG G GGG $\frac{1}{1}$ G GGG I ATC $^{\mathrm{C}}$ V GTC $^{\rm C}$ S TCC H FTTT H CAC A GCA S AGC N AAC V GTT Q CAG I ATC A GCC E GAG H CAC s TCC D GAC R AGG G GGA I ATT R AGA D GAT E GAG A GCT E GAG R AGG T ACA N AAT D GAC R CGA T ACG K AAG S AGC S TCT E GAA G GGC E GAG D GAT E GAG Γ V GTC GGA H CAC TACT V GTC GGG V GTG \overline{W} D GAC T ACA R AGG T ACG E GAA S AGC W TGG $^{\mathrm{C}}$ P CCA \overline{W} A GCC $^{\rm C}$ C TGC S AGT . 96C 9 99C M ATG A GCC G GGC N AAT N AAC D. GAC $^{
m Y}$ W TGG L CTG \mathbf{F} TTC S TCT D GAC L CTG FTTC H CAC L Q CAG TACC GGT $_{
m L}$ D GAT A GCC D GAC Q CAG R AGG G GGG R AGG S TCT င TGC $^{\mathrm{C}}$ V GTG D GAT G GGG $_{
m L}$ N AAC C TGC Q CAG 9 99C I ATC L CTG W TGG GGA A GCC Y TAT VGTG T ACA W TGG T ACC CTGT W TGG 990 TACA FTIC K AAG I ATT I ATA g GGC I ATC FTTC 9 990 R CGC V GTC 9 960 S TCT S TCC W TGG Γ P CCC S TCC E GAA E GAA A GCA I ATC L TTA FTTC K AAG GGG S TCA $\frac{1}{1}$ I ATA P CCT PCCT H CAT 9 Q CAA S TCA C TGC C R AGA A GCC A GCC T ACG D GAC GGG Q CAG G GGG K AAA $^{\rm C}_{
m TGT}$ I ATC T ACA L

Fig. 20



1253 3786 1273 3846 T ACC D GAC D GAC D GAT GGA $^{\rm C}$ GGA V GTG R CGT T ACA V GTG 9 9 9 9 R AGA \overline{W} I ATA S TCC R AGA 9 66C D GAT A GCA E GAA H CAC W TGG $^{\rm C}$ T ACA I ATC I ATC E GAG IGG V GTG ACC R AGA ⊟ E GAG . GGG E GAA S TCT GCA c TGC P CCA E GAG

1293 3906 $_{
m L}$ A GCT S TCT 9 Cာ ၁၅၅ Γ Q CAG Q CAG $_{\rm TGT}^{\rm C}$ VGTG VGTG E GAA A GCG E GAG A GCC $_{
m L}$ D GAC $\overline{\mathbf{W}}$ S TCC

1313 3966 M ATG D GAC D GAT $_{
m ITG}$ WTGG I ATC TACC GGA TACT G GGA Q CAG 9 990 \mathbf{F} S TCG A GCT D GAC R AGG $_{
m L}$ A GCC A GCT

1333 4026 S AGT Q CAG GGA W TGG PCCC K AAA A GCC H CAC $_{\mathrm{TGT}}$ D GAC WTGG L CTA \mathbf{F} $\mathbf{T}\mathbf{T}$ S TCA E GAG N AAT . GGA K AAA C TGC R CGG

1353 4086 Γ S TCA K AAA $_{
m L}$ s TCG Q CAG GGA S TCT C TGC R AGG V GTG 9 A GCT D GAT E GAA K AAG H GGA $^{\rm C}_{
m IGT}$ D GAC

1373 L L CTC L L G GGG F TTT I ATC S AGT S TCC L TTA I ATT L CTT A GCA L TTA H CAT GGT S TCA S TCC A GCC N AAT

4206 L PCCC $_{
m L}$ H CAT K AAA O CAA K AAA Q CAG V GTT R CGA ည် T W TGG T ACG L FTTT L CTA I ATT F TTT Γ V GTT

1413 T ACC GAG 됴 M ATG E GAG H CAT TIC ഥ LTTA N AAT E GAG E GAG L S TCT GGT R AGG R AGG R AGA T ACC S TCA V GTT R AGA

Fig. 2H

4628

1454 4389



1433 4326 1453 4386 T K ACA AAA ggH CAT A GCC N AAC CCC E ACC S TCT D GAC A GCC D GAT' PCCT s TCA LCTT P H G T R T CCA CAT GGG ACA AGA ACC L G V TTG GGA GTT $_{
m L}$ S D T S AGC GAC ACA TCG E D GAG GAC (A GCT R AGA D GAT E GAA $^{
m C}_{
m TGT}$

TGA

4626 4468 4547 CTTTAGACTTCCAGGGCTCACCAGATCAACCTCTAAATATCTTTGAAGGAGACAACAACTTTTAAATGAATAAAGAGGA AGTCAAGTTGCCCTATGGAAAACTTGTCCAAATAACATTTCTTGAACAATAGGAGAACAGCTAAATTGATAAAGACTGG

Fig. 21



what for more part - some of for some and some of the sold for the sold of the 641 681 561 241 281 321 361 401 441 481 521

Fig. 2J

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	10	0	20	30	40	50	09	70
Hum.	MMLPQNSWH	IDFGRCC	CHQNLFSAVV	TCILLLNSCF	LISSFNG	TDLELRLVNGD	Hum. MMLPQNSWHIDFGRCCCHQNLFSAVVTCILLLNSCFLISSFNGTDLELRLVNGDGPCSGTVEVKFQGQWG	OWG
	••	••	•	•	••	•••		•••
WC1	WC1 MAL	GR	-HLSLRGL	CVLLLGT	BAM	QALELRLKDGV	-HLSLRGLCVLLLGTMVGGQALELRLKDGVHRCEGRVEVKHQGEWG	EWG
			10	2	20	30	40	20
;	08	0	06	100	110	120	130	
Hum.	TVCDDGWNT	rastvvc 	KQLGCPFSFA	MFRFGQAVTR	-HGKIWL	DDVSCYGNESA	Hum. TVCDDGWNTTASTVVCKQLGCPFSFAMFRFGQAVTR-HGKIWLDDVSCYGNESALWECQHREWGSHN	SHN
WC1	TVDGYRWTLF	<pre></pre>	RQLGCGAAIG	- FPGGAYFGP	GLGPIWL	LYTSCEGTEST		 NDG
	09	0	70	80	06	100	110	
	140	150	160	170	180	0 190	200	
Hum.	CYHGEDVGVNCYGEAN	NCYGEAN	LGLRLVDGNN	SCSGRVEVKF	QERWGTI	CDDGWNLNTAA!	ILGLRLVDGNNSCSGRVEVKFQERWGTICDDGWNLNTAAVVCRQLGCPSSFISSG	SSG
147 C								••
ı, ĭ	INDGRUAGV	 	-rvklagedg 140	FCSGRVEVES	GEAWIPV	SDGNFTLATAQI	CAELGC	VLG
i i	120	<u></u>	140	150		160 170	180	
	.210	220	230	240	250	0 260	270	
Hum.	VVNSPAVLRPIWLDDI		LCQGNELALW	NCRHRGWGNH	DCSHNED	VTLTCYDSSDLE	LCQGNELALWNCRHRGWGNHDCSHNEDVTLTCYDSSDLELRĽVGGTNRCMGRVE	RVE
,	•	:	•	•	•			••
WC1	HELFRESSAQVWAEEF) VWAEEF.	RCEGEEPELW	VCPRVPCPGG	TCHHSGS.	AQVVCSAYSEVF	RCEGEEPELWVCPRVPCPGGTCHHSGSAQVVCSAYSEVRL-MTNGSSQCEGQVE	QVE
	190 .	200	210	220	2	230 240) 250	

Fig. 2K

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Hum.	280 LKIQGRWGT	290 HHKWNN	300 DVVCKQLGCG	310 TALHFAGLPH:	320 LQSGSDVVWLI	330 OGVSCSGNESI	340 TLWDCRHSGT
WC1	MNISGOWRALCZ 260	SHWSL 270	ANANVICRQLGCGVAISTPGGPHL 280 290	VAISTPGGPH. 290	CVEEGDQILT2 300	. ::::::::::::::::::::::::::::::::::::	TLWSCPVTAL
Hum.	350 360 VNFDCLHQNDVSVICS	350 360 370 380 390 400 410 VNFDCLHQNDVSVICSDGADLELRLADGSNNCSGRVEVRIHEQWWTICDQNWKNEQALVVCKQLGCPFSV	370 LELRLADGSNI	380 NCSGRVEVRII	390 HEQWWTICDQN	400 WKNEQALVVC	410 KQLGCPFSV
WC1	GGPDCSHGN 330	GGPDCSHGNTASVICS-GNQI- 330 340		 		QVLPQCND- 350	NDSV
Hum.	420 FGSRRAKPS	420 430 440 450 460 470 480 FGSRRAKPSNEARDIWINSISCTGNESALWDCTYDGKAKRTCFRRSDAGVICSDKADLDLRLVGAHSPCY	440 SCTGNESALWI	450 DCTYDGKAKR	460 ICFRRSDAGVI	470 CSDKADLDLF	480 LVGAHSPCY
WC1	: .:	. : GSA	ASEDSA	: PY		::: .: ::: CSDSRQLRLVDGGGPCA	:::: RLVDGGGPCA
	m	360		-	370	0,	380
	490	500	510	520	530	540	550
Hum.	GRLEVKYQG	GRLEVKYQGEWGTVCHDRWSTRNAAVVCKQLGCGKPMHVFGMTYFKEASGPIWLDDVSCIGNESNIWDCE	TRNAAVVCKQI	LGCGKPMHVFC	SMTYFKEASGE	IMLDDVSCIG	NESNIWDCE
	•••		•••••••••••••••••••••••••••••••••••••••	•	•••••••••••••••••••••••••••••••••••••••		
WC1	GRVEILDQG	GRVEILDQGSWGTICDDGWDLDDARVVCRQLGCGEALNATGSAHFGAGSGPIWLDNLNCTGKESHVWRCP	LDDARVVCRQI	LGCGEALNATO	SAHFGAGSGE	INTDNTNCLC	KESHVWRCP
	390	400	410	420	430	440	450

Fig. 2L



560 570 580 590 600 610 620 HSGWGKHNCVHREDVIVTCSGDATWGLRLVGGSNRCSGRLEVYFQGRWGTVCDDGWNSKAAAVVCSQLDC ::::::::::::::::::::::::::::::::::::	630 640 650 660 670 680 690 PSSIIGMGLGNASTGYGKIWLDDVSCDGDESDLWSCRNSGWGNNDCSHSEDVGVICSDASDMELRLVGGS :: :: :: :: :: :::::::::::::::::::::	700710720730740750760SRCAGKVEVNVQGAVGILCANGWGMNIAEVVCRQLECGSAIRVSREPHFTERTLHILMSNSGCTGGEASL.::.:::::::::::::::::::::::::::::::::	770 780 800 810 820 830 WDCIRWEWKQTACHLNMEASLICSAHRQPRLVGADMPCSGRVEVKHADTWRSVCDSDFSLHAANVLCREL : : : : : : : : : : : : : : : : : : :
60 570 SWGKHNCVHREDVIVT :::::::::::::::::::::::::::::::::::	640 LGNASTGYGK: . :. SVALREGFRP(710 JNVQGAVGILC . :: :.: ILDQGSWGTIC	780 RWEWKQTACHLNME. :: .: .: SWGWRQHNCNHQED. 670
Hum. WC1	Hum. WC1	Hum. WC1	Hum.

Fig. 2M

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Hum.	840 850 860 870 880 890 900 NCGDAISLSVGDHFGKGNGLTWAEKFQCEGSETHLALCPIVQHPEDTCIHSREVGVVCSRYTDVRLV-NG
WC1	LGHMPFRE, 40
Hum.	930 940 950 960 970 WGSLCDTHWDPEDARVLCRQLSCGTALSTTGGKYIGERSVRVWGHRFHCL
WC1	TSQCEGQVEMKISGRWRALCASHWSLANANVVCRQLGCGVAISTPRGPHLVEGGDQISTAQFHCSGAESF 810 820 830 840 850 860
Hum. WC1	1030 1040 LDNCQMTVLGAPPCIHGNTVSVICTGSLTQPLFPCLANVSDPYLSAVPEGSALICLEDKRLRLVDGDSRC : .::::::::::::::::::::::::::::::::
	880 890 900 910 920 930 940
Hum. WC1	1050 1060 1070 1080 1090 1100 1110 AGRVEIYHDGFWGTICDDGWDLSDAHVVCQKLGCGVAFNATVSAHFGEGSGPIWLDDLNCTGTESHLWQC .:::::::::::::::::::::::::::::::::::
	950 960 970 980 1000 1000 1010

Fig. 2N



1180 TAIAGIVCRQLG :::: DITVSVICRQLG	DR .: GRRPKSCPTAAA 1140	.300 .DASFGQGTGTIW .:.:::::::: .SAAFGPGNGSIW 1210	1350 1360 QSLKSLNASSGHLALI .::: :: TSNSLPGIFSLPGVLCLI 1280
NIT.	1190 1200 1210 1220 1230 1240 um. CGENGVVSLAPLSKTGSGFMWVDDIQCPKTHISIWQCLSAPWERRISSPAEETWITCEDR ::.:::::::::::::::::::::::::::::	1250 1260 1270 1280 1290 1300 umIRVRGGDTECSGRVEIWHAGSWGTVCDDSWDLAEAEVVCQQLGCGSALAALRDASFGQGTGTIW ::::::::::::::::::::::::::::::::::::	1310 1320 1330 1340 um. LDDMRCKGNESFLWDCHAKPWGQSDCGHKEDAGVRCSGQSLKSLNASSGHLALI :::::::::::::::::::::::::::::::::::
1160 1170 SSCAGRLEVFYNGTWGSVGRR :::::::::::::::::::::::::::::::::::	1230 VQCLSAPWERRIS ::::::	1280 MDLAEAEVVCQQ :.::::::::::::::::::::::::::::::::::	.csgvrttlptt
1140 1150 ICSEFTALRLYSETETE: ::::::::::::::::::::::::::::::::	1210 1220 12 WVDDIQCPKTHISIWQCLSAPWE::::::::::::::::::::::::::::::::::::	1270 HAGSWGTVCDDS ::::::::: HNGSWGTVCDDS	1310 1320 1330 1340 Hum. LDDMRCKGNESFLWDCHAKPWGQSDCGHKEDAGVRCSG ::::::::::::::::::::::::::::::::::
1130 HKEDAGVICSEF ::::::::::::::::::::::::::::::::::::	1200 LSKTGSGFMWVD . :: ::: GLREGSRPRWVD	1260 DTECSGRVEIW: .:::::::::::::::::::::::::::::::::::	1330 LWDCHAKPWGQ::::: :::: LWDCVAEPWGQ:
1120 1130 PSRGWGQHDCRHKEDAG ::::::::::::::::::::::::::::::::::::	1190 1200 Hum. CGENGVVSLAPLSKTGS ::::::: WC1 CGDSGSLNTSVGLREGS 1080 1090	1250 IRVRGGDTE .:::::: CTDREKLRLRGGDSE(1320 LDDMRCKGNESFLWDC ::: ::::: LDEVQCGGRESSLWDC 20 1230
Hum. WC1	1 Hum. CG :: WC1 CG 1080	Hum WC1 CT	1310 Hum. LD :: WC1 LD

Fig. 20

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1370 1380 1410 um. LSSIFGLLLLVLFILFLTWCRVQKQKHLPLRVSTRRRGSLEENLFHEME :::.::::::::::::::::::::::::::::::::	1420 1430 1430DTPNHGCEDASDTSLLGV . : .:::: : ::: : ::::::::::::::::::::	
1400 TRRRG :: LLTQKEGLGSP	1430 -DTPNHGCEDAS : :: REAANPGEGEESFWLLQC 1400 1410	
1390 QKHLPLRVS : : : SSYEDALAEAVYEELDY 1320 1330	1430 DTPNH : LNFSREAANP	-
1390 (QKHI : : RALSSYEDAI 1320	420 EDPHGTRTSD : .:.:. EKEDGVRSSQTGSF 380 1390	
1370 1380 Hum. LSSIFGLLLLVLFILFLTWCRVQK :::::::::::::::::::::::::::::::::::	1420 LKREDPHGTRTSD- : ::::: EEEVPPEKEDGVRSSQT	
1370 1. SSIFGLLLLVLFI: GSLLFLVLVILVT()0 1300	um. TC	0 EAT-K ·: PVTFS
Hum. LSSI ::: WC1 LGSL 1290	Hum. TC WC1 EVPVPGT 1360	1450 Hum. LPASEAT-K : .: .: WC1 LGTSPVTFS 1430

Fig. 2P

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PRADEMENTS

		•	
TCTCTG:::-	140 TTTGGA : ::: TCTGGA	210 TGGGGG ::::: TGGGGC	CCATTT : : GGAGCT
SAGAACCITITCTCTG :::::::::::::::::::::::::::::::::	130 TTAATGGAACAGAT :::: :: : TGGGTGGTCAAGCT	200 CAGGGACAG ::.::::::	270 CTTGGATGT ::::::: CTGGGGTGT
TGCTGTCAT(::::::	120 130 140 AGCAGTTTTAATGGAACAGATTTGGA :: ::: :::::::::::::::::::::::::::::	180 190 200 216 GGGACAGTGGAGGTGAAATTCCAGGGACAGTGGGG ::::::::::::::::::::::::::::::::	230 240 250 260 270 GGTGGAACACTACTGCCT—CAACTGTCGTGTGCAAACAGCTTGGATGT :::::::::::::::::::::::::::::::
TGGAAGATGC	110 TTTCTCATCA:::AC	180 GGACAGTGGA ::: ::::: GGAGAGTGGA	250 CAACTGTCGT ::.:::: CATCTGTAGT
ATATTGATTT	100 GAATTCCTGCTT : ::- CGGCA-	170 ccrgcrcrg: :::::	240 CTACTGCCT- : .: : TTGAAGGATG
AACTCGTGGC .:: ::: -GCTC-TGG-	90 CCTGCTCCT::::::::::::::::::::::::::::::	160 GGAGACGGTCC ::::::::	230 GGTGGAACA(:::::::::::::::::::::::::::::::::
<pre>Hum. ATGATGCTGCCTCAAAACTCGTGGCATATTGATTTTGGAAGATGCTGCTGTCATCAGAACCTTTTCTCTG ::: ::: ::: ::: ::: ::: ::: ::: ::: ::</pre>	80 90 110 120 130 140 Hum. CTGTGGTAACTTGCATCCTGCTCTTCTCTCATCAGCAGTTTTAATGGAACAGATTTGGA ::::::::::::::::::::::::::::::	150 160 200 210 Hum. GTTGAGGCTGATCAATGGAGCTCCTGCTCTGGGACAGTGGAGGTGAAATTCCAGGGACAGTGGGGG :::::::::::::::::::::::::::::::	220 230 240 250 260 270 Hum. ACTGTGTGATGATGGTGGAACACTACTGCCT-CAACTGTCGTGTGCAAACAGCTTGGATGTCCATTT ::::::::::::::::::::::::::::::::
ATGA:::ATG	CTGTC::::::::::::::::::::::::::::::::::	GTTG! :::: GCTG?	ACTG1 ::.:: ACAG1
Hum. WC1	Hum. WC1	Hum. WC1	Hum. WC1

Fig. 2Qi

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340 ATGATGTTTC . ::. :: TGTATACTTC 280 410 CTGTTATCAT	.:.::::	::::::::::::::::::::::::::::::::::::::	TGATGGGTGGA :::::::: TGATGGGAACT 480
280 330 340 Hum. TCTTTCGCCATGTTTTGGACAAGCCGTGACTAGACATGGAAAATTTGGCTTGATGTTTTC : : : : : : : : : : : : : : : : : : :	::::::::::::::::::::::::::::::::::::::	::::::::::::::::::::::::::::::::::::::	ď, Ω
320 CTAGACATGGAAAA :::::: CAGGACTTGGCCCC 260 390 ACACGGGAATGGG	: ::. AT-TCTAATATT 330 460 -TCTGGGTTTGA	::::::::::::::::::::::::::::::::::::::	CAAGAAAGGTGGGGGACTATATGTG:::::::::::::::
310 GCCGTGACTZ :::::.:. ATTTTGGGCCA(250 380 GGAATGTCAACZ	::::::::::::::::::::::::::::::::::::::	::::::::::::::::::::::::::::::::::::::	AAATTCCAAGA/ : .::: CATTCTGGA(
300 GTTTTGGACAAG :::::.: TGGAGGGGCTTA 240 370 TCAGCTCTCTGG	::::::::::::::::::::::::::::::::::::::	::::::::::::::::::::::::::::::::::::::	GAGTGGAGGTGAAAT: :::::::::::::::::::::::
290 :: :: :: :: :: :: :: :: :: :: :: :: ::	::::::::::::::::::::::::::::::::::::::	**************************************	AACTCCTGTTCAGGGA(:::::::::::::::::::::::::::::::::
280 Hum. TCTTTC : :: WC1 GCCATT 220 350 Hum. CTGTTA	::: WC1 ATGTG 290 420 Hum. GGAGA		Hum. AACTC .::: WC1 GAC-C

Fig. 20ii

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620 AGTTGT	: : Trggg	690 GCACT- :.:: -CTCTT	760 CTTGT : GG	830 AGAGCTGA ::: CCCTG- 650
O TCTTCTGGA	:.:: GCAGAGTTGGG 520	0 ATGAGTTGG ::::: ATGAG 560	750 GTCACATTAA: ::: TTCA	820 8 GGAGAGTAGAG CC
610 CTTTTATTT	CTGT	680 GCCAGGGGAATGAGT ::::::::- -CCTGGGACATGAG- 550 560	0 750 ATGAGGATGTCAC ::::::: -TGAAGAGTTCA-	0 CTGTATGGGC :.:: CAGAGTG
600 TCCATCTT	::::::::::::::::::::::::::::::::::::::	670 ATTTTATG(. : : TGT(740 AGTCACAA1 : : :	800 810 TGGAACTAACCGCTGTATGG :::: :::::-:::
590 ACTAGGATG		660 GCTGGATGACATT :::: :::: : GCTGTGTCTGT 540	730	800 FAGGTGGAACT ::::
580 STGCAGGCA	::: CAG	650 CCCATTTGGCTGG :::: AAGGCTG-	720 rgggaaat	790 !AAGGCTTG1 :: !CT
570 GCTGCCGTGGT	.:::: CACTGCC	630 670 680 690 TAATAGCCCTGCTGTATTGCCCCCATTTGGCTGGATGACATTTTGCCAGGGGAATGAGTTGGCACTT- ::: TTGTGGCAAGGCTGTGTCTGTCCTGGGACTGAGCTCTT 530 530	700 710 720 730 740 750 760 CTGGAATTGCAGACATCGTGGGGAAATCATGACTGCAGTCACAATGAGGATGTCACATTAACTTGT :.:.:::::::::::::::::::::::::::::::	770 780 800 810 820 830 TATGATAGTAGTGATCTTGAACTTAGGTGGAACTAACCGCTGTATGGGGAGAGTAGACTGA ::::::::::::::::::::::::::::::::::::
560 570 580 590 600 600 620 Hum. ACTIGAATACTGCCGTGGTGTGCAGCCAACTAGGATGTCCATCTTTTATTTCTTCTGGAGTTGT	.::.: .::::: TCACACTTGCCACTGCC 490 500	630 .um. TAATAGCCCTG ::.: WC1 TTGTGGC	700 CTGGAATTGCAGACATC :	770 TATGATAGTAGTGATC ::::::::::::::::::::::::::::::::::::
Hum.	WC1	Hum. WC1	Hum. WC1	Hum. WC1

Fig. 20iii

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900 CGTATGCAA	: .::. GTTCAGCAT 700	970 GATGTTGTA :.:: .: GGTGGAGAT 760	1040 GAACCGTCA ::: ATGCCA 820	1110 GGAACTGCGACT .:: .: ::: GACCAC-ACT 880
840 850 860 870 880 890 900 Hum. AAAICCAAGGAAGGAACGIATGTCGTATGCAAA	::::: :::: ::::: :::::::::::::::::::::	910 920 930 940 950 960 970 GCAGTTGGGATGTGGAACCGCACTTCACTTCGCTGGCTTGCCTCATTTGCAGGTCTGATGTTGTA .::::::::::::::::::::::::::::::::::	980 1000 1010 1020 1030 1040 TGGCTTGATGGTGTCTCCCGGTAATGAATCTTTTCTTT	1100 AGATTT
880 GAACAATGCT(.:.: :::: GATCTGCT- 0	950 CCTCATTTGC2 ::::::: CCTC-TCAG-7	1020 TTTGGGACTGG : ::: CTCCC-ACTGG	1090 CTCAGATGGAG ::: ::: CACCCCGGAG
870 ACCATAAGTG	:::: :::::::::::::::::::::::::::::::::	940 CGCTGGCTTG	1000 1010 10 GGTAATGAATCTTTTCTTTGGG ::: ::::::::::::::::::::::::::::::	1070 1080 AACGATGTGTCTGTGATCTGCTC : .:: :::::::::::::::::::::::::::::
860 SACCGTATGCC	: ::: : : : : : : : : : : : : : : : :	20 930 940 ACCGCACTTCACTTCGCTGGCTT :::::::::::::::::::::::::::	1000 GCTCCGGTAAT .:. ::.: ACAATGGAGAG	1070 AACGATGTGT : .:: .
850 GAAGGTGGGG	.::: 099 09955	920 ATGTGGAACCG .:.:: CAGAAGTCCGG	990 3GTGTCTCCTG ::: TCTG-GA	1050 1060 1070 1080 1090 ATTITGACTGTCTTCATCAAAACGATGTGTCTGTGATCTGCTCAGATGGAGC ::::::::::::::::::::::::::::::::::
840 AAATCCAAG	::: TCCA	910 um. GCAGTTGGGA' .:. WC1 ACTCZ		
Hum.	WC1	Hum. WC1	Hum. WC1	Hum. WC1

Fig. 2Qiv

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1120 1130 1140 1150 1160 1170 1180 AGCAGATGGAAGTAACAATTCAACAGTGGACAATATG :::::::::::::::::::::::::::::::::	1190 1200 1210 1220 1230 1240 1250 TGACCAGAACTGGAAGAATGAACAAGCCCTTGTGTAAGCAGCTAGGATGTCCGTTCAGCGTCTTT ::::::::::::::::::::::::::::::	1260 1270 1280 1290 1300 1310 1320 GGCAG-TCGTCGTGCTAAACCTAGAGCTAGAGACATTTGGATAAACAGCATATCTTGCACTGGG ::::.::::::::::::::::::::::::::::::	1330 1340 1350 1360 1370 1380 1390 AATGAGTCAGCTCTCTGGGACTGCACATAGGAAAAGCAAAGCGAACATGCTTCCGAAGATCAGATG :::::::::::::::::::::::::::::::::
1160 AGAATTCA-T :::::: CGATTTCACT 920	1230 AAGCAGCTAG :: ::: GCC-CTGG 970	1300 ATTTGGATAA : :: :: AGGTGCTTCC 1040	1370 13 CAAAGCGAACATGCTTCC :. :: :: :: :: :: CTCAGAGGACA-GCGCCC 1090 1100
1150 GTAGAGGTG :: .: CTAACAGCC	210 1220 CCCTTGTGGTTTGT/ :::::::	1270 1280 1290 130 AAACCTAGTAATGAAGCTAGAGACATTTGGATI: :: :: :: :: :: :: :: :: :: :: :: ::	1360 SATGGAAAAGC :: :GGCC
1140 TGTTCAGGGAGA ::.::: : TGATCAGATC 900	1210 ACAAGCCCTT ::: CCT-	1280 AGTAATGAA : : : ::: GCTCAGGAA 1020	1350 :::
1130 FRACAATTG1 .:. ::. FAAGGTGZ	1200 CTGGAAGAATGAA :::::. CTGTGGAGTTGT- 950	1270 TGCTAAACCT : .::::: TCTGTGATCT	1340 CTCTGGGACTGC .:.: .::: TACAGGCTCTGC
	1190 1200 TGACCAGAACTGGAAGAATGA .:.:: .:: .:::: AGTCCT-TCCTGTGGAGTTGT 940 950	1260 GGCAG-TCGTCGTC :::: :::: GGCAACACAGCCTC 1000	1330 1340 AATGAGTCAGCTCTCTGGGACTGCA ::::::::::::::::::::::::::::::::::::
Hum. WC1	Hum. WC1	Hum. WCl	Hum. WC1

Fig. 2Qv

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1460	AIGG :: CCGG 1160	ა :. ა	AG GG	SA CC
14	GGCC 11	;-AAT .:: .CGAT	TTAA : TCGG	CTGT(:: GTGC(
)))	. :::: . :::: :::: 	CAAGG	1590 CTATT : : TCACT	1660 CTGGGA ::
1450	.: : -GGTC 1150	1520 AGCACA: : GAC-CT	TGACC	TATCI
د د د	100-100 1-00-100	ATGG ::: CTGG	1580 TTGGTA :: . .CGGGGT	1650 GTCAAA::::::::::::::::::::::::::::::::::
1440	GACGGGG-GC140	1510 GACAG ::::: GACGG	15 rgrrr ccace	16 FGAGT :::: SGAGT
ىلىن ئالىلىلى	 GAC	TCATOR : : : TGATOR	OCATGI	0 GAAA1 :::: GAAAC 0
1430 TAAGGG		1500 TGTGTG .::: CATCTG	1570 CTATGCZ :	1640 CATTGGZ
1 1		19 GACTO	AAGCC	CTTG(::: ACTG(
1400 1410 1430 1430 1440 1450 1460 Hiim Chagaaghaannanghaangaaagaaannaagaagaagaagaagaagaagaagaag	cag-cag-cag-cag-cag-cag-cag-cag-cag-c	1470 1480 1500 1510 1520 Hum. GAGATTGGAGGTGAAATACCAAGGAGGAGGGGGGACTGTGTGTCATGACAGGTGGAGCACAAGG-AATGC ::::::::::::::::::::::::::::::::::::	1530 1540 1550 1560 1570 1580 1590 Hum. A-GCTGTTGTGTAAACAATTGGATGTGGA-AAGCCTATGCATGTGTTTGGTATGACCTATTTAAAG ::::::::::::::::::::::::::::::	1600 1610 1620 1630 1640 1650 1660 Hum. AAGCATCAGGACCTATTTGGCTGGATGACGTTTGCATTGGAAATGAGTCAAATATCTGGGACTGTGA ::::::::::::::::::::::::::::::::::
1420	::: CAGC	1490 AGAGTG(:::	GCTG	ATGA(: .:: ACAA(
0 72 م م ت	::: CAGG	1480 1 ATACCAAGGAGA :::::: IGACCAGGGCTC	1550 AATTGG :- :: AGCTGG	1620 GCTGG : ::: GTTGG
1410	CAG-	1480 ATACC ::: TGACC 1180	AACAA :: GGCAC	TTTGC:::::TCTGC
րդնդող	1 1 1 1 1 1 1 1 1 1	STGAA .: .	10 3TGTA 3TGCA 10	1610 sgaccta ::::: sgccca
1400 TAAT		1470 SAGATTGGAGGTGA ::::::::: SAGAGTGGAGATCC	1540 GTTGTGTGTA ::::::: GTGGTGTGCA(00 1610 AGCATCAGGACCTA1 :::::::::: AGGATCAGGGCCCA1
רקהאר	wc1 crcaga	AGATT :::: AGAGT	GCTG::::	10 : .GGAT
ر =	:: :: :: :: :: :: :: :: :: :: :: :: ::	lum. GF :: WC1 GF	1530 m. A- rcl cc 1230	1600 n. AAG(:: :1 CAG(
H	A	Hu! W(Hur W(Hur W(

Fig. 2Qvi

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1690 1700 1710 1720 1730 AGCATAATTGTACACAGAGGATGTGATTGTAACCTGCTCAGGTGATGCA ::::::::::::::::::::::::::::::::::::	1760 1770 1780 1790 1800 TGGTGGGCGCCAGCAACCGCTCGGAAGACTGGAGGTGTACTTTCAAGGAC ::::::::::::::::::::::::::::::::	1830 1840 1850 1860 1870 ATGACGCTGGAACAGTAAAGCTGCAGCTGGTGTGTGTAGCCAGCTGGACTG .:.:::::::::::::::::::::::::::::::::	1900 1910 1920 1930 1940 CATGGGTCTG-GGAAACGCTTCTA-CAGGATATGGAAAATTTGGCTCGATG : : : : : : : : : : : : : : : : :
1670 1680 1690 1700 1710 1720 1730 um. ACACAGTGGAAGCATAATTGTGTACACAGAGGATGTGATTGTAACCTGCTCAGGTGATGCA : ::::::::::::::::::::::::::::::::::	1740 1750 1760 1770 1780 1790 1800 ACATGGGGCCTGAGGCGCGCCAGCACCGCTGCTCGGGAAGACTGGAGGTGTACTTTCAAGGAC : :::::::::::::::::::::::::::::::::::	1810 1820 1830 1840 1850 1860 1870 Hum. GGTGGGCACAGTGTGTGATGACGCTGGAACAGTAAAGCTGCAGCTGGTGTGTAGCCAGCTGGACTG ::::::::::::::::::::::::::::::::::::	880 1890 CCCATCTTCTATCATTGG:.: TGGGGACAGTGGAACC 1580 1
Hum. WC1	1 Hum. WC1	Hum. WC1	1 Hum. WC1

Fig. 2Qvii

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2010 GAAATAATGAC :.::::: GGAATTACAAC 1700	2080 3CTTGTGGG :: :::.	2150 rgrgcraar :::::::	2220 sggrcrcca	: ::: ::: CCTGGACGCCA 1900
2000 GGTGGGGA :. TGACCCTTGG 1690	2070 FGGAGCTGAG :::: GATCCGC-	2140 GGAATTCTG: :::::::::::::::::::::::::::::::::::	2210 CTGCAATCAG	.:: BAAGCCCT
1990 2 CATGCAGGAACAGTGG : ::: .:: : CTGGCAGTGTCCTTCT 1680	2060 -CATCGGATA' ::::::	2130 AGGGTGCCGT(:::: :: :: AGGGCTCCTG(2200 rgaatgtgggj	:. ::::: GGCTGTGGA(1890
1980 CTGGTCATGC :: :: :: CTCTGGC	2050 2060 2070 ATCTGTTCTGATG-CATCGGATATGGAGCTGAGG ::::::::::::::::::::::::::::::::::	00 2110 2120 2130 2140 2150 CTGGAAAAGTTGAGGTGCCGTGGGAATTCTGTGTGTTAA ::::::::::::::::::::::::::::::::::::	2190 GCAGGCAACT	GTGTGTGTGCAAGCAGCTGGGCTGTGGAGAAGC 1870 1880 1890
1970 19 TGAGTCAGATCTCT :.: ::::: ACTGACACCTCTCT 1660 1670	2040 GGAGTG-ATC :: ::: AGCCTATATC 1730	2110 AAAAGTTGAG .:.::::: GAGAGTGGAG	2180 GAAGTTGTTT	::::: CGTGTGGTGT(1870
1950 1960 1970 IGTTTCCTGTGATGAGATGAGTCA :::::::::::::::::::::::::::::::::::	2020 2030 2040 CAGTCACAGTGAAGATGTTGGAGTG- :: ::: ::: :: :: CATGCTCTCCAAAGGAGGAAGCCTAT 1710 1720 1730	2100 GGTGTGCTGG : :: ::: GCTGCTCTGG	2170 GAACATTGCT	:::::: TGGACGATGCC 0 1860
1950 1960 1970 1980 2000 2010 um. ATGTTTCCTGTGAGATGAGTCAGATCTCTGGTCATGCAGGAACAGTGGGTGGGGAAATAATGAC	2020 2030 2040 2050 2060 2070 2080 um. TGCAGTCACAGTGAAGATGTTGGAGTTTCTGATGCATTGTGGG :::::::::::::::::::::::::::::::	2090 2100 2110 2120 2130 2140 2150 Hum. TGGAAGCAGCTGCTGGAAAAGTTGAGGTGAATGTCCAGGGTGCCGTGGGAATTCTGTGTGCTAAT ::::::::::::::::::::::::::::::::::		::::: GCTGGGACC 185
Hum. 7 WC1 -	Hum. T : WC1 T	Hum. T(: WC1 T(Hum. G	WC1 C

Fig. 2Qviii

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2230 2240 2250 2260 2270 2230 n. GAGA-GCCTCATTTCACAGAAAGAACATTACACATCTTAATGTCGAATTCTGGCTGCACTGGAGGGGA	.:. :: :: :: :: ::::: .:::::::::::::::	2300 2310 CTCTCTGGGATTGTATACGA	. : :	2360 2370 2380 TTTGATCTGCTCAGCCCACAGGCCCA	. : ::::::::::::::::::::::::::::::::::	2430 2440 2450 2460 2470 2480 2490 Hum. GTGAAACATGCAGACACATGGCGCTCTGTCTGTTCTCTCTTCTTCATGCTGCCAATGTGCT	::: :: :: :: :: :: ::: ::: ::: ::: :::
Hum.	W	Hur	W(Hum.	M	Hum	WC

Fig. 2Qix

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	2500	2510	2520	2530	2540	2550	2560
Hum.	GTGCAGAGA	ATTAAATTGI ::::	GGAGATGCCF	GTGCAGAGAATTAAATTGTGGAGATGCCATATCTCTTTCTGTGGGAGATCACTTTGGAAAAGGG-AATGG	TGTGGGAGATC	ACTTTGGAAA	AGGG-AATGG
WC1		TGGGATGI	GGCAAGGCTG	GTGCAGAGCTGGGATGTGGCAAGGCTGTGTCT-GTCCTGGGACACATGCCATTCAGAGAGTCCGATGG	TGGGACACATG	SCCATTCAGAG	AGTCCGATGG
2180	08	2190	2200	2210	2220	2230	2240
	2570	2580	2590	2600	2610	2620	2630
Hum.		GGCCGAAAAG	TICCAGIGIC	TCTAACTTGGGCCGAAAAGTTCCAGTGTGAAGGGAGTGAAACTCACCTTGCATTATGCCCCATTGTTCAA	AACTCACCTTG	SCATTATGCCC	CATTGTTCAA
	•		••••••		•••	•••••••••••••••••••••••••••••••••••••••	••
WC1		GGCTGAAGAG	TTCAGGTGTG	CCAGGTCTGGGCTGAAGAGTTCAGGTGTGATGGGGGGGGG	GCCTGAGCTCT	GGTCCTGCCC	CAGAGTGCCC
	2250	2260	2270	2280	2290	2300	2310
	2640	2650	2660	2670	2680	2690	2700
Hum.	CATCCGGAA	GACACTTGTA	TCCACAGCAG	CATCCGGAAGACACTTGTATCCACAGCAGAGATGGTTGGAGTTGTCTGTTCCCGATATACAGATGTCCGAC	STIGICIGITC	CCGATATACA	SATGTCCGAC
		•••	••••••		••	••	
WC1	TGTCCAGGA	GGCACATGTC	TCCACAGTGG	WC1 TGTCCAGGAGGCACATGTCTCCACAGTGGAGCTGCTCAGGTTGTCTGTTCAGTGTACACAGAAGTCCAGC	STTGTCTGTTC	AGTGTACACA	SAAGTCCAGC
	2320	2330	2340	2350	2360	2370	2380
	2710	2720	2730	2740	2750	2760	2770
Hum.	TTGTGAATG	GCAAATCC	CAGTGTGAC	TTGTGAATGGCAAATCCCAGTGTGACGGGCAAGTGGAGATCAACGTGCT-TGGACACTGGGGGCTCAC	AGATCAACGTG	CT-TGGACAC	regegereac
		•	••		•	•	•••
WC1		ACGCCACCTC	TCAATGTGAG	TTATGAAAAACGGCACCTCTCAATGTGAGGGGCAGGTGGAGAT-GAAGATCTCTGGACGATGGAGAGCGC	4GAT-GAAGAT	CTCTGGACGA	rggagagcgc
	2390	2400	2410	2420	2430	2440	2450

Fig. 2Qx

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<u> </u>	E E.			
2840	CTCI	2910 CTTA :::	2980 AATA ::::	3050 ACCC : :: AACC
	GACTG : AGTCG 2520	::::: :::::: :cacrG	.argga .::: .arggc. 2660	3040 3050 AATGTATCTGACCC::::::::: TTCCTGTCTCAACC 2730
30	regg)0 TTTC/ TTTC/ 20	10 11 11 12 12 13 13 13 13 13 13 13 13 13 13 13 13 13	0 GTA1 :.: CTG1
2830	10101 11101 10101	2900 AGGTT	2970 GTATC(:::	3040 AAATG
	TCAG TCGG	: : : AGCC()	CCCT(:::GACT(2650)	TCGC, .:. ACGA(2720
2820	CAGC	2890 TGGGG	2960 CACCT(.:::	3030 ATGCCT .::
2	:: :: :CGT(28 77670 17070	25 AGC <i>I</i> .: .	30 CCAT : .: CAGI
	*ATGCAC :: CTGTCC 2500	CGTGT(:: CAGAT(TTGGA : ::. TGGGT 2640	GTTTC:: : GCCCC:
2810	TTCI ::: TTGI	60 2880 2900 29 ATATATTGGAGAAAGAAGTGTTCGTGTGTGGGACACAGGTTTCATTGCT : : : : : : : : : : : : : : : : : : :	2950 GTTC:	3020 3030 CACTGTTTCCATGCCTCGCA .:: :: :: :: TGCTGCCCCAGTGCAACGAC
	: .:: : .:: : CAATG 2490	.::.: .::.: .GGAGG	.rgaca ::::. rgacr	CCAGC
00	1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1	70 5AAA(:::. 5AAG(10 NAATC :	0 BACCC ::::
2800	AGA:	2870 GGAGAJ : .::	2940 GTCAA ::: . GTCCT	3010 CCTGA ::::
	CAGA : TGGC(2480	.: .: .CTTG(AACT : : AGTT 2620	GAAG :::. GAAA 2690
2790	<pre>GGACCCAGAAGATGCCCGTGTTCTATGCAGACAGCTCAGCTGTGGGACT ::.::::::::::::::::::::::::::::::::</pre>	2860 AAATA : :	2930 2940 2950 2960 2970 29 TGGATAACTGTCAAATGACAGTTCTTGGAGCACCTCCCTGTATCCATGGAAA :: .::: :::: :::::::::::::::::::::::::	3000 3010 CACAGGAAGCCTGACCCAGC :::::::::::::::::::::::::::::::
7	CTGG CTGG CTGG	23 3GAA3 5.:: 3GAC0	2: :TTCT(: :: TCCT(3(3) 3) 3) 3) 3) 3)
	::::: ::::::::::::::::::::::::::::::::) \GGAGG; \.::: \AGAGG; 2540	CACTT	GATCT ::::: GATCT 2680
2780	ACAC	2850 CACA(: : CCCC/	2920 GAGT :::: GAGT	2990 CTGT :::: CTGT
	<pre>TGTGTGACACCCACTGGGACCCAGAGGTGCCCGTGTTCTATGCAGACAGCTCAGCTGTGGGACTGCTCT : :::::::::::::::::::::::::::::::::</pre>	2850 2860 2870 2880 2890 2900 2910 CTCAACCACAGGAGAAATATTTGGAGAAAGAAGTGTTCGTGTGGGGACACAGGTTTCATTGCTTA :::::::::::::::::::::::::::::::::::	2920 2930 2940 2950 2960 2970 2980 GGGAATGAGTCACTTCTGGATAACTGTCAAATGACAGTTCTTGGAGCACCTCCCTGTATCCATGGAAATA :::.::::::::::::::::::::::::::::::	2990 3000 3010 3020 3030 3040 3050 CTGTCTCTGTGATCTGACCCCCAGCCACTGTTTCCATGCCTCGCAAATGTATCTGACCCCCCCC
	Hum. WC1	Hum. WC1	Hum. WC1	Hum. WC1

Fig. 2Qxi

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		3070	3080	3090	3100	3110	3120
Hum. WC1	ATATTTGTCTGCAGTTCCAGAGGGCAGTGCTTTGATCTGCTTAGAGGACAAACGGCTCCGCCTAGTGGAT	FTCCAGAGGGC ::::::: CCTCAGAGGAG	AGTGCTTTGA :::::: AGTTCTCCCT	ATCTGCTTAGAGGACAAACGGCTCCGCCTAGTGGA ::::::::::::::::::::::::::::::::::	GACAAACGG :: AGCAGGCAGG	CTCCGCCTAG' :::::::: CTCCGCCTGG	rggat :::: rggac
	2740 2750	2760	2770	2780	2790	2800	
Hum.	3130 GGGGACAGCCGCTGTG	3140 FGCCGGGAGAG	3140 3150 3160 3170 3180 3190 3190 3190	3160 CACGACGGC1	3170 TCTGGGGCA	3180 CCATCTGTGA	3190 16ACG
7				· · · · · · · · · · · · · · · · · · ·) •• (
) 3	2810 2820	2830 2830	2830 2840 2850 2860 2850 2860 2870	19400466601 2850	CC16666CA6	CATCTGTGA: 2870	l'GAT'G
	3200	3210	3220	3230	3240	3250	3260
Hum.	GCTGGGACCTGAGCGA	SATGCCCACGT	TGCCCACGTGTGTGTAAAAGCTGGGCTGTGGAGTGGCCTTCAATGCCACGGT	AAGCTGGGCTG	TGGAGTGGC	CTTCAATGCCA	ACGGT
WC1	ACTGGGACCTGGACGA	RECCCETET	TGCCCGTGTGGTGTGCAGCTGGGCTGTGAAAGCCTTTAAAAAAAA			Z ン つ む 由 立 本 々 o 由 し c	
 		2900	2910	2920	2930	2940	D D D
	3270	3280	3290	3300	3310	3320	3330
Hum.	CTCTGCTCACTTTGGGGAGGGGTCAGGGCCCATCTGGCTGG	GGAGGGGTCA	GGCCCATCTG	GCTGGATGAC	CTGAACTGCA	ACAGGAACGG	GTCC
		•••		••••••	•••	•••	••
WC1	GTCTGCTCACTTCGGG	GGCAGGATCA	GCAGGATCAGGCCCCATCTGGCTGGACGACCTGAACTGCACAGGAAAGGAGTCC	GCTGGACGAC	CTGAACTGCA	ACAGGAAAGGA	GTCC
٠	2950 2960		2980	2990	3000	3010	

Fig. 2Qxii

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3350 3360 3370 3380 3390 3400 CTTCCCGCGGCTGGGGCACGCACGCACGCACGGGGTCA ::::::::::::::::::::::::::::::::::::	3410 3450 3460 3470 CAGTGAAACTGAAGAGCTGTGCTGGGAGATTGGA .:::::::::::::::::::::::::::::::::::	3530 3540 TAGCAGGCATTGTG .: .: .: CTGTGTCCGTGATC 3210	3560 3570 3580 3590 3600 GTGGGGAGAATGGAGTTGTCAGCCTCGCCCCTTTATCT-AAGACAGGCTCTG:::::::::::::::::::::::::::
0 ACAAGGAGC ::::::: ACAAGGAGC	0 GAGCTGTGC :::::: CAG-TGTGC	3520 3530 CATCACCACAGCCATAGCAGG :::: .: .: .: .: .: .: .: .: .: .: .	0 IATCT-A :. ::: : ITGGTCTCA 3270
3380 ACTGCAGGCA(::::::::::::::::::::::::::::::::	3450 TGAAACAGAG :: 3AGGACCAGC	3520 AACATCACCA(::: . CCCATGGAAG)	3580 3590 STIGTCAGCCTCGCCCTTTA .::: :: :: :: AGTCT-CAACACCTCTGTTGG
3370 GGCAGCACG ::::::::: GGCGCACG	3440 SAGTGAAAC ::::: : -GGTGAG-CC	3510 GCAGGAGGA :: :: GCCGCAGCC	3580 TGTCAGCC1 .::::
3360 :::::::::::::::::::::::::::::::::::	3430 TGAGGCTCTAC : ::: : TCAGGAT	3490 3500 3510 ACCTGGGGCAGCGTCGGCAGGAGAA ::::::::::::::::::::::::::::	3560 3570 GTGGGGAGAATGGAGTT :::::::::::::::::::::
3350 CCCTTCCC :::::::::::::::::::::::::::::	3420 34 ACAGCCTTGAGGCT .::::::: CTGGCCCTCAGGAT 0 3110	3490 GGACCTGGG :::::::: GGACCTGGG	3560 CTGTGGGGA ::::::: ATGTGGGGA 3240
3340 3350 3360 3370 3380 3390 3400 CACTTGTGGCAGTGCCGCTGGGGGCAGCACGACTGCAGGCACAAGGAGGACGCAGGGGTCA ::::::::::::::::::::::::::::::::::::	3410 3420 3430 3440 3450 3460 3470 TCTGCTCAGAATTCACAGCCTTTACAGTGAAACTGAAACAGAGAGTGCTGGGAGATTGGA :::::::::::::::::::::::::::	3480 3490 3510 3520 3530 3540 um. AGTCTTCTATAACGGGACCTGGGCAGCGTCGGCAGGGAACATCACCACAGCCATAGCAGGCATTGTG .::::::::::::::::::::::::::::::::	3550 3560 3570 3580 3590 3600 Hum. TGCAGGCAGCTGTGGGGAGAATGGAGTTGTCAGCCTCGCCCCTTTATCT-AAGACAGGCTCTG ::::::::::::::::::::::::::::::::
Hum. WC1	Hum. WC1	Hum. A WC1 G 3150	Hum. T' : WC1 T' 3220

Fig. 2Qxiii



Fig. 2Qxiv

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•			
3840 3850 3860 3870 3880 3890 3900 Hum. GGAAGTGGTGTCAGCAGCTGGCTGTTGGCTTGCTTGGCTGCCCTGAGGGACGCTTCGTTTGGCCAG :::::::::::::::::::::::::::::::::	3930 3940 3950 3960 3970 'GGTTGGATGACATGCGTGCAAAGGAAATGAGTCATTTCTATGGGACTGTCACG :::::::::::::::::::::::::::::::::::	3980 3990 4000 4010 4020 4030 4040 um. CCAAACCCTGGGGACAGACTGTGGACACAAGGAAGATGCTGGCGTGAGGTGCTCTGGACAGTC : .:::::::::::::::::::::::::::::::::::	4050 4060 4070 4080 4090 um. GCTGAAATCACTGAATGCCTCCTCAGGT-CATTTAGCA-CTTATTTATCCA . :::::::::::::::::::::::::::::::::::
3890 SCCCTGAGGGA(::::::: SCCGTGCGGTCT	3960 ATGAGTCATTTC : :::: : GGGAGTCCTCC(0 3990 4000 4010 4020 4030 4040 CCAAACCCTGGGGACAGACACAAGGAAGATGCTGGCGTGAGGTGCTCTGG : .:.:::::::::::::::::::::::::::::::::	4080 -CATTTAGCA- :.:::: rcrcccrGGCAI
3880 CTGCTCTGGCTG :::::::	0 3920 3930 3940 3950 GGAACTGGAACCATCGGTTGGATGACATGCGGTGCAAAGGAAAT ::::::::::::::::::::::::::::::::::	4020 AGGAAGATGCT ::::::::: AGGAGGATGCT	4070 CCTCAGGT(::::::::::::::::::::::::::::::::::
3860 3870 CAGCTGGGCTGTGGCTCT ::::::::::::::::::::::::::::::::::	3940 ATGACATGCGGT : :: ::::: ACGAGGTGCAGT 60 3670	4010 CTGTGGACACAA ::::::: CTGCAAGCACGA	TGCCT : ::. GGACCAGAACA 30
3860 TGTCAGCAGCTG :::::::::::::::::::::::::::::::::::	10 3930 CCATCTGGTTGGAT ::::::::::: GCATCTGGCTGGAC 3650 3660	10 4000 GGGACAGAGTGACT ::::::::::::::::::::::::::::::::::::	4050 4060CTGAAATCACTGAATGCCT- :: : : : : : : : : : : : : : : : :
0 GGAAGTGGTGTGTCAG ::::::::::::: TGAGGTGGTGTGTCAG 3570 3580	3910 3920 Hum. GGAACTGGAACCATCT :::::::::::::::::::::::::::::::	3980 3990 Hum. CCAAACCCTGGGGACA : .:.::::::: WC1 CGGAGCCCTGGGGGCA 3710 3720	4050 GCTGAAA' . : . :: AACATTGCCCACGA 3780 3790
3840 Hum. G(WC1 T(3910 Hum. G(: WC1 G(3980 Hum. Co WC1 Co	Hum. G WC1 A

Fig. 2Qxv

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Hum.	9	4100 TATCTT-	i 1	-CTTCTC	4110 -TGGGCTC-CTTCTCCTGGTTCT	4130 4140 GTTTATTCTATTTCTCA	4140 FTCTCA
[3]	:	**** ** ** ** ** ** ** ** ** ** ** ** *					•• [
₹ >	3850	3860	3870	3880	3890	10016616ACTCACCTACTCA 3870 3880 3890 3890 3900 3910	'ACT'CA
		4150	4160	4170		4180	
Hum.		CGTGGTGCCGAGTT	TCAGAAACAAAAACATCT-	AACATCT	>>> · · ·	GCCCCTCAGAGTTT	
WC1		GATGGAGAGCAGAGCG	GCAGAGCCTTAI	CCAGCTAT	GAAGATGCTCTI	CAGAGCCTTATCCAGCTATGAAGATGCTCTTGCTGAAGCTGTGTATGAGGAGCT	GAGCT
	3920	3930	3940	3950	3960	3970 3980	
		4190	4200		4210	4220	
Hum.	1	CAAC	-CAGAAGGAGGG-	GTTCT	-CTCGAGG	GTTCT-CTCGAGGAGAATTTATTCCATGA	
W.		? ?	::·:::::::::::::::::::::::::::::::::::		* : : : : : : : : : : : : : : : : : : :	######################################	E 4 4
) :	3990	4000	4010	4020	4030 4030	4040 4050	AAAAT
	4230		4	4240		. 4250	
Hum.	GATGGAG-	3GAG	B	-ACCTG	CCTC-	AAGAGAGAGAC	AGGAC
	••	••••••	•	••	••		••
WC1	TATGAT	SATGCTGAAG	SAAGTACCAGTG	CCTGGAAC	ICCTICICCCIC	TATGATGATGCTGAAGAAGTACCAGTGCCTGGAACTCCTTCTCCCTCTCAGGGGAATGAGGAGGAAGTGC	AGTGC
	4060	4070	4080	4090	4100	4110 4120	

Fig. 2Qxvi

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ı v	E E	
4260 4270 um. CCACATGGGACAAGAACCTCAGA-TGACACCCCCAA :::::::::::::::	4310 umCCATGGTTGTGAAGATGCTAGCGACAC	
.: :: CCTGAACTTC	4320 ATCG : AAAGGGGATG	,
4280 CTCAGA-TGACACCC ::::::::::::::::::::::::::::	.c: : ccaggggaag	ACAAAA TTCTCG
4280 CTCAGA- :::::: TCCTCTCAGAC	4310 -TGCTAGCGACAC : ::::: CTTCTGGCTGCTC	4350CCTCTGAAGCCACAAAA :::::::: ATCCCCAGTGACTTTCTCG 0
.: : cggggTgAGG 4150	43 GAAGAT ::::: GAAGAGAGCT 4220	TGC :: TGGGAACATC 4290
4270 Hum. CCACATGGGACAAGAAC ::::::::::::::::::::::::::::	4310CCATGGTTGTGAAGATGCTAGCGACAC ::.:::::::::::::::::::::::::::::::::	4340 4350 um. CTTCCTGCCTCTGAAGCCACAAA :: :::: ::::::::::::::::::::::::
4260 . CCACAT :: :: 1 CCCCAG 4130	CC :: 1 TAATCC	. CTT :: 1 GTTGAA
Hum WC	Hum. WC1	Hum. WC1

Fig. 2Qxvii

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12 67 32 127 52 187 92 72 247 112 367 132 427 152 487 172 547 G GGG S AGC A GCA D GAT P CCA E GAA V GTT T ACC GGA \mathcal{O} W TGG A GCG R AGG GGT D GAT S AGT $_{
m L}$ $^{\rm C}$ GAG ഥ P T ACC R CGT S AGT Q CAG K AAG V GTC A GCT M ATG D GAC T ACG E GAA L CTG I ATC K AAA R CGT GIC PCCT > L CTG T ACG D GAT L D GAT R AGA I ATC s AGC K AAG 9 9 9 9 P GGG $_{
m L}$ $_{
m ITG}$ D GAC F TTC $^{\mathrm{F}}$ D GAC L $_{
m L}$ A GCA TACT A GCC S AGT N AAC A GCC E GAG A GCC $_{
m L}$ Y TAT D GAC Γ A GCC F TTC \mathbf{F} TTC S TCG PCCA Γ YTAC FTTT I ATT PCCA $^{\rm C}_{
m IGT}$ T ACC I ATC L R AGA D GAT Q CAG A GCC WTGG Q CAG 9 9 P A GCC LCTT Q CAG V GTC E GAA P T ACA C $_{
m L}$ M ATG L CTG R AGG LCIC R CGA I ATA E GAG TACC L CTG GTCGACCCACGCGTCCGGTCTGTGGCTGAGC Q CAA CCC 9 9 A GCT M ATG N AAT Y TAC Y TAC F TTC M ATG K AAG G GGG N AAC S AGC L S TCC L P Q CAG VGTG K AAG K AAG H CAT D GAT F TTC G GGG H CAC Y TAC L CTA K AAG T ACC Q CAA LCIT Q CAG F TTC LCTC R AGG K AAG V GTC LCTT 9 G GGG FTTC TACT P N AAT FTTT E GAA $_{
m L}$ 9 S AGC N AAT V GTC A GCC Y TAC I ATT LCTC LCTT GGA G GGA GGG $_{\mathrm{TGT}}^{\mathrm{C}}$ S TCT F TTC

Fig. 3A



192 607 M ATG GGG D GAT V GTG $_{
m ITG}$ V GTC A GCT T ACG H CAT K AAG H CAC AGCT CCC D GAC F TTT P S AGC K AAA

212 667 L T ACA R CGC M ATG $_{
m L}$ I ATC P E GAG S AGT 9 9 9 9 L FTTC N AAC N AAC M ATG TACT GGT S TCT Y TAT L

232 727 S TCC A GCC D GAC H CAT H CAT L CTG W TGG R CGC LCTC F TTC N AAC D GAC TACC K AAG L CTC V GTC PCCT Q CAG S TCC GGA

252 787 S AGC A GCC T ACA E GAG E GAG FTTC FTTC $^{
m F}$ Y TAC VGTC V GTC Q CAG TACC S TCG P I ATC A GCC A GCA V GTG F TTT

272 847 D GAC N AAT K AAG C TGC V GTC R AGA A GCT V GTG R CGG S TCG T ACA H CAC LCTC R AGG E GAG F TTT FTTC D GAC \mathbf{F} $\mathbf{T}\mathbf{T}$ E GAG

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292 907 L $_{
m L}$ Q CAG A GCC K AAG $_{
m L}$ FTTC TACC T ACC WTGG K AAG K AAG Q CAG $_{
m L}$ $_{
m L}$ K AAG E GAA . ⁵ 9 V GTG

312 967 A GCC PCCC L L CTG V GTC A GCG H CAC R I ATC V GTC N AAC $^{
m F}$ P $_{
m L}$ Q CAG G GGG P CCG Q CAG TACC

> C TGC

(

332 1027 G GGG 9 V GTT Q CAG W TGG Q CAG S TCC TACC FTTC V GTC A GCA Y TAC I ATC H CAC P A GCT T ACA PCCC S TCT D GAT

352 1087 GGG Ŋ K AAG F TTT V GTC R CGT E GAA I ATT D GAC $\frac{1}{1}$ L CTC S TCT F TTC A GCC $_{\rm TGT}^{\rm C}$ V GTT A GCG S TĊT S AGC R AGG TACC

Fig. 3B

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372¹ 1147 T ACC E GAG PCCT 9 R AGG TACT T ACT W TGG R S TCA TACT E GAA K AAA N AAC GAG K AAA K AAA

392 1207 M ATG FTTC TACC $_{\rm L}$ A GCC K AAG D GAT S TCT S TCC P 9 V GTG S TCA C TGC S AGT . 9 P CCA R CGG P N AAC

412 9 9 S TCT K AAA VGTG L CTG L CTG P T ACG G GGG V GTG V GTG Q CAA E GAG D GAT M ATG L CTG $_{
m TTC}$ H CAT D GAC K AAG

432 L H CAT S AGC H CAC GGG D GAT L CTT 9 9 Q CAG A GCC T ACA E GAG V GTG A GCA L CTT R CGG T ACA $^{
m Y}$ E GAG V GTG

47 / 95 452 1387 S AGC D GAC G GGG S AGT VGTA V GTG A GCT K AAG H CAC L S TCG GGG T ACA TACC T ACC GGA L CTG Y TAC M ATG V GTC

472 1447 $_{
m L}$ N AAC R GGC V GTT PCCT E GAA PCCT D GAC PCCT F TTC LCTG Q CAG I ATT E GAG E GAA V GTG $_{
m L}$ H CAT A GCT S AGT

492 V GTG R AGG WTGG V ĞTC G GGT GGA S TCA FTTC 9 9 V GTA F TTT VGTG A GCA GGT Q CAG TACC PCCC A GCC Γ Q CAG

512 567 P D GAC R CGG A GCC L V GTC $^{\mathrm{C}}$ D GAC V GTG $^{\mathrm{C}}$ S AGC E GAG Y TAT V GTC S AGT $^{\rm C}$ N AAC A GCC R CGA PCCC

532 1627 N AAC L CTG N AAC PCCC A GCC S TCT $_{
m L}$ LCTC C TGC $^{\mathrm{C}}$ TACC R CGA S TCC E GAG PCCT D GAC W TGG A GCC $^{\rm C}$ H CAC

Fig. 3C

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(



552 1687 592 1807 572 1747 612 1867 1927 652 1987 672 2047 632 692 2107 712 M ATG P S AGT L CTG S TCA E GAA A GCC A GCC GCT Ø P V GTC W TGG $\frac{1}{1}$ ${
m F}$ ${
m TTT}$ PCCT GGG F TTT R CGG GGC A GCT Y TAT L 9 96C D GAT GGT LCTC L CTC S AGT L CTG Y TAT S TCC N AAT $_{
m L}$ S AGT V GTC A GCA A GCC V GTC S TCT GGC E GAG A GCC V GTC TACT R AGA $^{\rm C}$ A GCC E GAA N AAT TACT L CTG R AGG V GTC $\frac{1}{1}$ A GCA K AAA L TTG YTAC A GCA TACC TACC TACT P CCA W TGG I ATT A GCC V GTC \overline{W} Q CAG $\frac{L}{TTG}$ V GTC S TCC E GAG I ATC S TCA T ACT $^{\rm C}$ D GAC P A GCC F TTT PCCA L CTG Q CAA S Q CAG Q CAG GTG V GTC H CAC > N AAC PCCG H CAC S TCT Y TAC K AAG S AGC CCC LCIC G GGG P A GCC RCGC LCTC D GAC V GTG \overline{W} I ATC R CGG S AGC C TGC E GGT V GTG I ATC H CAT Y TAC E GAG Q CAG PCCC P CCA G GGG W TGG E GAG S TCC LCIC M ATG PCCT LCIC V GTC V GTT Y TAC R CGG Q CAG A GCC D GAC R CGG E GAG A GCA GGA S TCC PCCC Q CAG GGA Q CAG $_{
m L}$ LCTT A GCA D GAT I ATC IATC A GCC S TCA K AAG S AGC I ATC P CCA Q CAG V GTG 9 9 A GCT LCTT WR AGG S TCC 9 99C V GTG PCCT A GCA $_{\rm CTG}$ V GTG S TCC S AGC N AAC H CAT I ATA $\overset{Y}{\text{TAC}}$ $_{
m L}$ L TTA A GCC

Fig. 3D



732 2227	752 2287	762 2317
R AGA	D GAC	
S AGC	A GCT	
L TTA	D GAC	
PCCG	V GTG	
A GCC	D GAT	
K AAG	S AGT	
E GAG	AGCC	
GGG	S TCT	
P CCT	T ACC	
RCGC	R AGG	
L CTG	C TGC	V A * GTA GCT TAA
TACC	E	A GCT
E GAG	K AAG	V GTA
C TGT	PCCC	E GAG
9 9	S TCT	T ACT
Q CAG	Q CAG	9 990
V GTT	L	L CTA
K AAG	H CAC	C TGC
9	Q CAA	N AAC
R CGG	E GAG	N AAC

2554 2633 2791 2870 TGACAGCAGCACAAAAGACCACCTTTCTCCCCTGAGAGGAGCTTCTGCTACTCTGCATCACTGATGACACTCAGCAGGG CCAGACCTGCTCCTACACTGATATTGAAGAACCTGGAGAGGATCCTTCAGTTCTGGCCATTCCAGGGACCCTCCAGAAA CACAGTGTTTCAAGAGATCCTAAAAAACCTGCCTGTCCCAGGACCCTATGGTAATGAACACCAAACATCTAAACAATC TGATGCACAGCAGTCTGCCTCCCCTATGGGACTCCCTTCTACCAAGCACATGAGCTCTCTAACAGGGTGGGGGCTACCC ATATGCTAACATGCCACTCCTGGAAACTCCACTCTGAAGCTGCCGCTTTGGACACCAACACTCCCTTCTCCCAGGGTCA TGCAGGGATCTGCTCCCTCCTGCTTCCCTTACCAGTCGTGCACCGCTGACTCCCAGGAAGTCTTTCCTGAAGTCTGACC **ACCTITCTTCTTGCTTCAGTTGGGGCAGACTCTGATCCCTTCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCCTTCT**

Fig. 3E

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70 DEDTLLLS	140 SYNVTHLY ::.::: SYNATHLY 140	210 SEPILMR:::::: SEPILMR	280 GGEKLLQ :::::: GGEKLLQ 280
60 SFFHQKGLQI SEFQQKGLRI 60	130 :FNFIRVLVS :::::::::::::::::::::::::::::::::::	190 200 210 AVLVDGMLYSGTMNNFLGSEPILMR::::::::::::::::::::::::::::::::::::	270 VARVCKNDV ::.:::: VAQVCKNDV 270
20	90 100 110 120 140 LALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLY ::::::::::::::::::::::::::::::::::::	190 ITAVLVDGMLY ::::::::	230 240 250 260 270 2 WLHHDASFVAAIPSTQVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKL ::::::::::::::::::::::::::::::::::::
40 3GQGPMPRVR3 :::::::: 3GQGPMPRVK3 40	110 PASDRKKSECA :::::::::	180 SQSPFDPAHKF :::. SQSPLTLFTS1 180	250 FFFEETASEF::::::::::::::::::::::::::::::::::::
30 LLEPTTTAGGC : ; LPSLPPASGTC 30	100 PRLKNMIPWE::::::::::::::::::::::::::::::::::::	170 SEDKVMEGKG ::::::: LIDKVMDGKG	240 AAIPSTQVVY :::::::::::::::::::::::::::::::::::
20 GLFLFQLLQI .:.::.: RVFFFQLFLI 20	90 LALDIQDPGV :::::::: LALNIQNPGI	160 ELQDSYLLPI :::::::: ELQDSLLLPI 160	230 RWLHHDASFV :::::::: RWLHADASFV 230
10 20 30 40 50 60 70 MALPALGLDPWSLLGLFLEQLLQLLLPTTTAGGGGQGPMPRVRYYAGDERRALSFFHQKGLQDFDTLLLS ::::::::::::::::::::::::::::::::::	80 100 110 120 130 140 GDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKSNETQCFNFIRVLVSYNVTHLY .::::::::::::::::::::::::::::::::::::	150 160 170 180 190 200 210 TCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTAVLVDGMLYSGTMNNFLGSEPILMR .::::::::::::::::::::::::::::::::::::	220 230 240 250 260 270 280 TLGSQPVLKTDNFLRWLHHDASFVAAIPSTQVVYFFFEETASEFDFFERLHTSRVARVCKNDVGGEKLLQ :::::::::::::::::::::::::::::::::::
Hum. Mur.	Hum. Mur.	Hum. Mur.	Hum. Mur.

Fig. 3F

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350 DIERVF ::::: DIERVF 350	420 TTRLAV ::::: TTRLAV 420	490 'SGGVW :::::	560 ILRPQS : ::
니 단	370 380 390 400 410 420 TYRGPETNPRPGSCSVGPSSDKALTFMKDHFLMDEQVVGTPLLVKSGVEYTRLAV ::::::::::::::::::::::::::::::::::::	440 450 460 470 480 490 LGTTTGSLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGAVFVGFSGGVW :::::::::::::::::::::::::::::::::::	510 520 530 540 550 560 CVLARDPHCAWDPESRTCCLLSAPNLNSWKQDMERGNPEWACASGPMSRSLRPQS::::::::::::::::::::::::::::::::::::
310 320 330 340 VLLPADSPTAPHIYAVFTSQWQVGGTRSSAVCAFSL ::::::::::::::::::::::::::::::::::::	400 KDHFLMDEQVV(:::::::: KDHFLMDEHVV(400	470 FPDPEPVRNLQI :::::::: SPDSEPVRNLQI 470	540 SWKQDMERGNPE :::::::: PWKQDMERGNPE 540
320 SPTAPHIYA: :::: SPSVSRIYA: 320	390 SSDKALTEM:::::::	460 AHLVEEIQL: ::::::	530 CLLSAPNLN: :::
310 RHAVLLPAD :::::::: RHAVLLPAD 310	380 RPGSCSVGP :::::::: RPGSCSMGP,	440 450 GTTTGSLHKAVVSGDSSA :::::::::::::::: GTSTGPLHKAVVPQDSSA 440 450	520 AWDPESRTC ::::::: AWDPESRLC 520
	370 TTYRGPETNP ::::::::::::::::::::::::::::::::::::	440 CLGTTTGSLH ::::::::: CLGTSTGPLH 440	
290 KKWTTFLKAQLLCTQ :::::::::::: KKWTTFLKAQLLCAQ 290	360 KGKYKELNKETSRWT ::::::::::: KGKYKELNKETSRWT	430 ETAQGLDGHSHLVMY :.:.:::::::::::::::::::::::::::::::::	500 RVPRANCSVYESCVD ::::::::::::: RVPRANCSVYESCVD 500
Hum. Mur.	Hum. Mur.	Hum. Mur.	Hum. Mur.

Fig. 3G

630	ENG	••	3NG		((00/	4LI	•	/LT							
_	CWATI	•••	CVATI		•		VLSG2		VLLG							
620	Hum. RPQIIKEVLAVPNSILELPCPHLSALASYYWSHGPAAVPEASSTVYNGSLLLIVQDGVGGLYQCWATENG		Mur. PPQLIKEVLTVPNSILELRCPHLSALASYHWSHGRAKISEASATVYNGSLLLLPQDGVGGLYQCVATENG	620	Ç	000	FSYPVISYWVDSQDQTLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWPHFVTVTVLFALVLSGALI		Mur. YSYPVVSYWVDSQDQPLALDPELAGVPRERVQVPLTRVGGGASMAAQRSYWPHFLIVTVLLAIVLLGVLT	069	760	EVA	••	EVA	160	
O	VQDGV	••	PQDGV		(O	FVTVT	••	FLIVT		7	NCLGT	•	NHLGA		
610	SLLLI	•	SLLLL	610	C	000	SYWPH	•••	SYWPH	089	750	/DADNI	••	/DADNI	750	
9	IVYNG	••	LVYNG		Ţ	õ	LAAQO	•	TAAOR		7.	SASD	••	SASD		
009	PEASS	•	SEASA	009	0.00	2	3GGAA1	•	SGGASI	019	740	PKECRI		KDHR	740 . 750	_
)9	PAAVI	••	SRAKIS		ί,	ò	LTRV	•••	PLTRV	•	77	HLQSE		HLQPS	1-	
590	/YWSH	::	(HMSH	290		2	SHVKVE		RVQVE	099	730	ILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRTSASDVDADNNCLGTEVA		Mur. LLLASPLGALRARGKVQGCGMLPPREKAPLSRDQHLQPSKDHRTSASDVDADNNHLGAEVA	730	
5	SALAS		SALAS	_,	ÿ	5	GIPRI	•	AGVPRI	v	73	GEKAI	•••	REKA		
0	CPHLS		CPHLS	580	C	2	DPELA	•••	DPELA	650	0	ETLRE	••	GMLPF	720	
580	ILELE		ILELR	u)	n C)	QTLAI		QPLAI	O	720	KVQGC		KVQGC	7	
0	AVPNS		TVPNS	570	c	>	VDSQD		VDSQD	640	0	LRARG		LRARG	710	
570	IKEVL	•••	IKEVL	5	079	7	WISYW	•••	WYSVV	9	710	SPLRA	••	SPLGA	7	
	RPQI	::	PPQL	260			FSYP	••	YSYP	630		ILVA	•	LLLA	700	
	Hum.		Mur.	Σ			Hum.		Mur.	<u>,</u>		Hum.		Mur.	7(

Fig. 3H

															•
30	CTGTGGCTGAGCATGGC		GGGGTCTGTACTGCTGGGGAACCATCTGGTGACCATCTCAGGCTGACCATGGC	02 09	60 70 80 90 100 TGGACCCCTGGAGCCTCTGGGCCTTTTTCCTTCCAACTGCTTC-AGCTGCT	: :::: .::::	130	170	CGGGGGGGGGCGCCCATGCCCAGGGTCAGATACTATGCAGGGAT	: ::::: :: ::::::::::::::::::::::::	200	240	CITCITCCACCAGAAGGGCCTCCAGGATTTTGACACTCTGCTCCTGAGTGGTG	CTTCTTCCAACAAAAGGCCTCCGAGACTTTGACACGCTGCTCCTGAGTGACG	270
20	1	••	GACCATCTC	50	90 TCTTCCAAC	::::::::::::::::::::::::::::::::::::::	120	160	GGGTCAGAI	GAGTCAAAT	190	230	TGACACTCT	TGACACGCT	260
	CGICCGGI-	••••••	ACCATCTGGT	40	80 GGCCTTTTCC	: :::	110	150	CCCATGCCCA	::::::::::::::::::::::::::::::::::::::	180	220	TCCAGGATTT	TCCGAGACTT	250
0	ACG		ACTGCTGGGGA	30	70 SGAGCCTCCTG	::::::::::::::::::::::::::::::::::::::	100	140	sceecaaeee	STGGTCAGGGG	170	210	CAGAAGGGCC	CAAAAAGGCC	240
10	<u> </u>		AGGGGTCTGT;	20	60 CTGGACCCCT	CAGGACTCATO	06	130	SCGGGGGGAG	: ::: . ::: FCTGGGACTG(160	200		SCTTCTTCCAZ	230
	Hum. GTCG-AC-CC		CTCGGACGCCTGGGTTA	10	40 50 Hum. CCTCCCAGCCCTGGGCC	CCTACCATCCCTGGGCCAGGACTCATGGAGTCTCCTGCGTGTTTTTTTT	80	110 120	GCTGCCGACGACGACCG	Mur. ATCACTGCCACCTGCTT	.0 150	180 190	Hum. GAACGTAGGGCACTTAG	Mur. GGGCACAGGGCCCTCAG	.0 220
102 ES	Hum.		Mur.		Hum.	Mur.			Hum.	Mur.	140		Hum.	Mur.	210

Fig. 3I

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270 280 290 300 310 GTGGGGGCTCGAGAAGCCATTCTGGCCTTGGATATCCAGGATCCAGGGTCCC	::::::::::::::::::::::::::::::::::::::	340 360 370 380 TACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTTAAGAAGAAG :::::::::::::::::::::::::::	410 420 430 440 450 TTTCAACTTCATCCGGTTTCTTACAATGTCACCCATCTCTACACCT :::::::::::::::::::::	460 470 480 490 500 510 520 Hum. GCGCCACCTTCACCTTCATTGAACTTCAAGATTCCTACCTGTTGCCCATCTC :::::::::::::::::::::::::::::::
300 GATATCCAGG	.:::::::::::::::::::::::::::::::::::::	370 GTGAATGTGCC ::::::::: CCGAATGTGCC 400	440 CAATGTCACCC :::::::::::::::::::::::::::::::::	460 470 480 490 500 510 520 GCGCCACCTTCACCTTGTACCTTCATTGAACTTCCTACCTGTTGCCCATC :::::::::::::::::::::::::::::::::
290 FICTGGCCTTG	: :::::: rccrggccrrg 320	360 CAGAAAAAGA ::::::::: SAGAAAAAGA 390	430 CTGGTTTCTTA ::::::::::::::::::::::::::::::::	500 TTGAACTTCAA :::::::::::::::::::::::::::::::
280 CGAGAAGCCA:	::::::::::::::::::::::::::::::::::::::	350 CAGCCAGTGA(:::::::: CAGCCAGTGA(380	420 CATCCGTGTCC ::::::::: CATTCGAGTCC	490 TGTACCTTCA1 ::::::::: TGTACCTTCA1 520
270 ACGTGGGGGCT	::::::: \TGTGGGGGCT 300	340 saraccerecc :::::::: saracccrecc	410 GTTTCAACTT ::::::::::::::::::::::::::::::	480 CAGCCCTGCT :::::::::
250 260 ATGGAAATACTCTCTAC	:::: :: :::::: ATGGCAACACTCTCTAT 0 290	320 330 CAGGCTAAAGAACATGA ::::::::::::: AAGGCTAAAGAACATGA 50 360	390 400 AGCAATGAGACACAGTG :::::::::::::: AGCAATGAGACACAGTG 0 430	460 470 GCGGCACCTTCGCCTTC : ::::::::::::::::::::::::::::::::
250 Hum. ATGGA	:::::: Mur. ATGGCAAC 280	320 Hum. CAGGC' :::: Mur. AAGGC' 350	390 400 Hum. AGCAATGAGACACAGTG :::::::::::::::::::::::::::::::::::	460 Hum. GCGGC2 : :: Mur. GTGGG2

Fig. 3J

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	530	540	C	550	260	570	580	590	
Hum.	GGAGGACAAGGTCATG	AAGGTCA!	TGGAGGGA	AAAGGCC	AAAGCCCCT	TTGACCCCGC	TCACAAGC	GAGGGAAAAGGCCCAAAGCCCCTTTGACCCCGCTCACAAGCATACG-GCTGTCTT	
		••		•••		•••	•••		••
Mur.		AAGGTCA.	rggacgg,	AAGGGCC	AAAGCCC-T	TTGACCCTG1	TCACAAGC	GATAGACAAGGTCATGGACGGGAAGGGCCAAAGCCC-TTTGACCCTGTTCACAAGCACACAAGCTGTCTT	
r)	260	570	280	5	290	009	610	620	
	009	, J	610	000	ر د د	019	0.10	O.	
Hum.	GGT	SGGATGC1	rc PCTATTCT(GGTACTA	TGAACAACT	TCCTGGGCAG	TGAGCCCA	TATICIGGTACTATGAACAACTICCIGGGCAGTGAGCCCATCCTGATGCGCACA	_
		•••		••	•••				
Mur.	GGTCGATC	GGATGC1	TTATTCC	GGCACCA	TGAACAACT	TCCTGGGCAG	GAGCCCA	GGTCGATGGGATGCTTTATTCCGGCACCATGAACAACTTCCTGGGCAGCGAGCCCATCCTGATGCGGACA	
	630	640	650		099	029	089	069	1
	.049	39	089	069	700	710	720	730	
Hum.	CTGGGATC	CCAGCCI	GTCCTCA	AGACCGA	CAACTTCCT	CCGCTGGCTG	CATCATGAC	Hum. CTGGGATCCCAGCCTGTCCTCAAGACCGACAACTTCCTCCGCTGGCTG	7.0
	•••	•••	•••	•••	••			•••	
Mur.		CCATCCI	GTTCTCA	AGACTGA	CATCTTCTT	ACGCTGGCTG	CACGCGGA	CTGGGATCCCATCCTGTTCTCAAGACTGACATCTTCTTACGCTGGCTG	<i>r</i> h
	700	710	720		730	740	750	760	
	740	750	9.0	760	770	780	790	800	
Hum.		CCTTCG	ACCCAGGT	CGTCTAC	TTCTTCTTC	GAGGAGACAĞ	CCAGCGAG	CAGCCATCCCTTCGACCCAGGTCGTCTACTTCTTCGAGGAGACAGCCAGC	_
		•••	•••	•••	•••	•••	•••		
Mur.	CAGCCATI	CCATCCE	ACCCAGGTO	CGTCTAT	TTCTTCTTT	GAGGAGACAG	CCAGCGAG1	CAGCCATTCCATCCACCCAGGTCGTCTATTTCTTTTGAGGAGACAGCCAGC	_
	770	780	790	-	800	810	820	830	

Fig. 3K

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810 820 830 840 850 860 870 870 850 860 870 8AGGCTCCACACATCGCGGGTGGCTAGAGTCTGCAAAGAATGACGTGGGCGGCGAAAAGCTGCTGCTGCAGAAG	::: :::::::::::::::::::::::::::::::	880 890 900 910 920 920 940 AAGTGGACCACCTTCCTGAAGGCCCAGCTGCTCTGCACCCAGCCGGGGCAGCTGCCCTTCAACGTCATCC :::::::::::::::::::::::::::::::::	0	GCCACGCGGTCCTGCTCCCGCCGATTCTCCCACAGCTCCCCACATCTACGCAGTCTTCACCTCCCAGTG	: ::::::::::::::::::::::::::::::::::::	0 1040 1050 1060 1070 1080 CAGGAGCTCTGCGGTTTGTGCCTTTAAG	::::::: GTCTTTAAA 0
860 GAAAAGCTG	::::::: GAAAGCTGC' 900	0 900 910 920 930 940 CTGAAGGCCCAGCCGGGGCAGCTGCCCTTCAACGTCA ::::::::::::::::::::::::::::::::::::	970	1000 AGTCTTCAC	::::::: AGTCTTTACC 1040	1070 ATTGAACGT	::::::::::::::::::::::::::::::::::::::
850 GTGGGCGGC	. ::::::: GIGGGCGGIG	920 CGGGGCAGC :.:::::	096	990 CATCTACGC	::::::::::::::::::::::::::::::::::::::	1060 TCTCTTGGAC	:::. :::: CTCACGGAC 1100
840 CAAGAATGAC	:::::: AAGAACGAC 880	910 TGCACCCAGC ::::: :::: TGCGCTCAGC	950	SAGCICCCCA	.: :::. rgrrrcccg	50 1. SCCTTCTCT	:::::::: 3CCTTCTCT 1090
O 8 AGAGTCTGC	.:::::: CAAGICIGC 870	OAGCTGCTCT	940	TCTCCCAC	::::::: FTCTCCCTC' 1010) 3CGGTTTGTGC	::::::::::::::::::::::::::::::::::::::
830	:::::: AGGGTGGCTC 860	900 rgaaggccca :::::::	930	y / g ccccccat	::::::::::::::::::::::::::::::::::::::	1040 AGGAGCTCTG	::::::::::::::::::::::::::::::::::::::
820 ACACATCGG	: : :: ATATATCC/ 850	890 CACCTTCC1	920	GICCIGCIC	:::::: GTCCTGCTG	1030 GCGGGACCP	::::::: GCGGGACCA 1060
			910	GCCACGCG	::::::::::::::::::::::::::::::::::::::	1020 103 Hum. GCAGGTTGGCGGGAC	::::::::::::::::::::::::::::::::::::::
Hum.	Mur.	Hum. Mur.		Hum.	Mur.	Hum.	Mur.

Fig. 31

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1090 1100 1110 1120 1130 1140 1150 GGGAAATACAAAGAACTTCACGCTGGACTACTTATAGGGGCCCTGAGACCACCCCC :::::::::::::::::::::::::::	1140 1150 1160 1170 1180 1180 1200 1210 1220 AGTGGGCCCCTCCTCTGATAAGGCCCTGACCTTCATGAAGGACCATTTCCTGAT .:::::::::::::::::::::::::::::::::::	1240 1250 1280 1290	GGGACGCCCCTGCTGGTGAATCTGGCGTGGAGTATACACGGCTTGCAGTGGAG::::::::::	1320 1340 1350 1360 ATGGGCACAGCCATCTTGTCATGTACCTGGGAACCACCACAGGGTCGCTCCACA ::::::::::::::::::::::::::::::::
1130 SGACTACTTA ::::::::::	1160 1200 3GCCTGACC .:::::::	1230		1340 rgraccrggg :::: :::: rgrarcrggg 1370
1120 ACTTCACGCTC	1150 1190 CCTCTGATAAC	1220	SCTGGTGAAA' ::::::::::::::::::::::::::::::::::	1330 CATCTTGTCA: :::::::::::::::::::::::::::::::::::
1110 ;AACAAAGAA? ::::::::	1140 1180 3TGGGCCCCT(::::::::	1210	<pre>.3</pre>	1320 :GGGCACAGCC ::: :::::
1090 1100 GGGAAATACAAAGAGTTG::::::::::::::::::::::		1200 1240	GGATGAGCAAGTGGTGGG :::::::::::::::::::::::::::::	1300 1310 ACAGCCCAGGGCCTTGAT .::::::::::::::::::::::::::::::::::::
		1190	\sim	m
Hum. Mur.	11 Hum. Mur.		Hum. Mur.	Hum. Mur.

Fig. 3M



		-	··.	
1370 1380 1390 1400 1410 1420 1430 AGGCTGTGGTAGGAGAGAGAGTTCAGCTGTTCCCTGACCCTGAACC	::::::::::::::::::::::::::::::::::::::	1440 1450 1460 1470 1480 1490 1500 TGTTCGCAACCTGCAGCTCCCCCCCCCCCCCCCCCCCCC	1510 1520 1530 1540 1550 1560 1570 GTGCCCCGAGCCAACTGTAGTGTCTTATGAGAGCTGTGTGTG	1580 1590 1600 1610 1620 1630 1640
1420 AGCTGTTCCCI	::::::::::::::::::::::::::::::::::::::	1490 CTTCTCAGGAG:::::::::::::::::::::::::::::	1530 1540 1550 1560 1 GTAGTGTCTATGAGACTGTGGACTGTCCTTGCCCGGGACCCC : ::::::::::::::::::::::::::::::::	1600 1610 1620 1630 1640 GAACCTGTTGCCTCTGCCCCCAACCTGAACTCCTGGAAGCAGGACA :: :::::::::::::::::::::::::::::::::
1410 GGAAGAGATTC	:::::::: GGAGGAGATTC 1440	1480 GTGTTTGTAGG :::::::: GTGTTTGCAGG	1550 TGGACTGTGTC :::::::: TGGACTGTGTG	1620 TGCCCCCAACC :: : ::: TGGCTC-TACC 1650
1400 GCTCATCTGGT	::: ::: :: GCTTATCTCGT 1430	1470 cccagggrgca :::::::::	1540 FGAGAGCTGTG ::::::::: CGAGAGCTGTG 1570	1610 rgccrccrgrc .::::::::
1390 GGACAGCAGT	::::::: GGACAGCAGT 1420	1460 CTGGCCCCCA(:::::::: CTGGCCCCCG(1490	1530 GTAGTGTCTA: : :::::: GCAGTGTCTA(1600 ccgaaccrgrr :: :: aagacrcrgcz 1630
1380 TGGTAAGTGG	::::. : . TGGTGCCTCA 1410	1440 1450 GTTCGCAACCTGCAG :::::::::::: GTTCGAAACCTGCAG 0 1480	1510 1520 GCCCCGAGCCAACT :::::::::::::::::::::::::::::::::	1580 1590 CCTGGGACCCTGAGTC ::::::::::::::::::::::::::::::::::::
1370 Hum. AGGCTG	:::::::: Mur. AGGCTGTGGTG(1400 141(1440 Hum. TGTTCG :::::: Mur. TGTTCG	1510 Hum. GTGCCCC :::::: Mur. GTTCCCI	1580 Hum. CCTGGG ::::: Mur. CCTGGG
		7	വ	•

Fig. 3N

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11		1660	1670	1680	1690	1700	1710
in in		AACCCAGAGIC	GAG1666A161666	GCCAGIGGCCCCAIGAGCAGCCII	I GAGCAGGAG))))))	TCAGAGCCGC
Mur.		PACCCGGAGTO	SGGTATGCACC	CGTGGCCCCA1	reccaegae	CGGCGT	AGAGCCCC
	1680	0691	00/1	1/10	1720	1/30	1740
	1720	1730	1740	1750	1760	1770	1780
Hum.	CCGCAAATCATTAAAG		CTGGCTGTCC	CCAACICCAIC	CTGGAGCTC	AAGTCCTGGCTGTCCCCAACTCCATCCTGGAGCTCCCCTGCCCCCCACCTGTCAG	CCTGTCAG
Mur.	CCTCAACTAATTAAAG	TTAAAGAAGTC	CTGACAGTCC	CCAACTCCATC	CTGGAGCTGC	**************************************	CCTGTCAG
	1750	1760	1770	1780	1790	1800 18	1810
	1790	1800	1810	1820	1830	1840	1850
Hum.	CCTTGGCCTCTTATTA		AGTCAIGGCCC	AGCAGCAGTCC	CAGAAGCCT	TTGGAGTCATGGCCCAGCAGTCCCAGAAGCCTCTTCCACTGTCTACAATGG	TACAATGG
			•••		•••		••
Mur.	CACTGGCCTCTTACCA 1820 1830		AGTCATGGCCG2 1840	AGCCAAAATCT 1850	TCAGAAGCCTC 1860	CTGGAGTCATGGCCGAGCCAAAATCTCAGAAGCCTCTGCTACCGTCTACAATGG 1840 1850 1860 1870 1880	CTACAATGG 1880
	1860	1870	1880	1890	1900	1910	1920
Hum.	CTCCCTCTTGCTGATA		AGGATGGAGTT	GGGGTCTCTZ	ACCAGTGCTG	CTGAGA	ATGGCTTT
Mur.	CICCCICIIGCIGCIG	CIGCIGCCGCA	AGGATGGTGTC	SGGGCCTCTA	ACCAGTGTGT	CCGCAGGATGGTGTCGGGGGCCTCTACCAGTGTGTGGGGGACTGAGAACGGCTAC	ACGGCTAC
	1890	1900	1910	1920 1	1930 1	1940 19	1950

Fig. 3C

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Hum.		1930 1940 1950 1960 1970 1980 1990 TCATACCCTGTGATCTCCTACTGGGTGGACAGCCAGGACCCAGACCCTGGCCTGGATCCTGAACTGGCAG	1950 STGGGTGGACA	1960 AGCCAGGACCA	1970 AGACCCTGGCC	1980 CTGGATCCTG	1990 AACTGGCAG
Mur.	::::::::::::::::::::::::::::::::::::::	::::::::::::::::::::::::::::::::::::::	:::::::: FTGGGTAGACA 1980	:::::::: AGCCAGGACCA 1990	::::::::::::::::::::::::::::::::::::::	::::::::::::::::::::::::::::::::::::::	:.:::::: AGCTGGCGG 2020
Hum.	2000 201 GCATCCCCGGGAGC	2010 GGAGCATGTG	0 2020 2030 2040 2050 2060 ATGTGAAGGTCCCGTTGACCAGGTCAGTGGTGGGGCCGCCCTGGCTGCCCAGCA	2030 Gaccagggto	2040 AGTGGTGGG	2050 ccecccreec	2060 TGCCCAGCA
Mur.	.:.: :::: GCGTTCCCCG 2030	::::::::::::::::::::::::::::::::::::::	::::::::::::::::::::::::::::::::::::::	::::::::::::::::::::::::::::::::::::::	.:.::::: :GGAGGCGGAG 2070	: :::: CTTCCATGGC 2080	::::::::::::::::::::::::::::::::::::::
Hum.	2070 208 GTCCTACTGGCCCCA	2080 CCCCACTTTGI	0 2090 2100 2110 2120 2130 CTTTGTCACTGTCATCATCATC	2100 GTCCTCTTTG	2110 CCTTAGTGCT	2120 TTCAGGAGCC	2130 CTCATCATC
Mur.	::::::::::::::::::::::::::::::::::::::	::::: ::: : : : : : : : : : : : : : :	::: ::: :::: ::::: ::::: :::::::::::::	::::::: GTCCTCCTGG 2130	::::::::::::::::::::::::::::::::::::::	.::: CCTGGGAGTG 2150	:::: :::::::::::::::::::::::::::::::::
Hum.	2140 215 CTCGTGGCCTCCCCA	2150 CCCCATTGAGA	0 2160 2170 2180 2190 2200 TTGAGAGCACTCCGGGCTCGGGGCTTCAGGGCTGTGAGACCCTGCGCCCTG	2170 CTCGGGGCAA	2180 GGTTCAGGGC	2190 TGTGAGACCC	2200 TGCGCCCTG
Mur.	::: : :::::: CTCCTCGCTTCCCCA 2170 2180	::::: :::: ccccacrgggg 2180	::.:::::::::::::::::::::::::::::::::::	::::::::::::::::::::::::::::::::::::::	::::::: GGTTCAGGGC 2210	:::::: : : : : : : : : : : : : : : : :	:::::: TGCCCCCA 2230

Fig. 3P



Fig. 3Q



2550 3GGGCT ::::	CCAG:::.	3GTA:::.	2750 :TGAA :: :TAGA :20
: : :	.CCATT(TTGAC(2580	2680 CAGGACCCTATGGTA .::: ::::: -GGGATTCTGTGGTG	2750 CACTCTGAA :::::::: CACTCTAGA 2720
0 .GGG1	2610 CTGGCC ::. TTGATT	2680 ACCC' : :	-CCA :: GICA
2540 AACAG	2610 CAGTTCTGG ::::: TGATTTTGA 570	CAGG .:: -GGG	2740 AAACT : .:: ACGCT
CTCT	TCAG; TTGA; 2570	2670 CTGTCCCA ::::: CTGTCT-G	0 TCCTGGAAACT-C:::::: TCCTGAACGCTGT 2710
2530 'GAGCT(2600 AGGATCCTT ::::::: AGGTTTCTT 60	2670 CCTGT ::::	0 :::: ::::
25 ACATGA ::: ACATT- 2510	2 GGAT :::: GGTT	CCTGCC:	2730 CACT(:.:: CTCCAT(
GCAC:::3	0 SAGAG . :: AC-AG(2560	2660 AAAAACC' :::. AAAGGTG' 2630	. :
500 2510 2520 2530 2540 2550 ccrargegacretarcagegegegerres::::::::::::::::::::::::::::	570 2580 2590 TACACTGATA-TTGAAGAACCTGGAG : .::. : ::::::: TGTGCTGTGACAGGAAGAGCCAGAC- 2540 2550 25	2630 2630 2680 2680 2680 2630 2630 2630 2630 2630 2630 2630 263	690 2700 2710 2720 2730 2740 2750 ATGAACACCAAACATCTAATGCTAA-CATGCCACTCCTGGAAACT-CCACTCTGAA : .::::::::::::::::::::::::::::::::::
::::::::::::::::::::::::::::::::::::::	GAAC	:0 ;ATCC] ;:::; ;A-CC?	A-CATO . : : .TTCCTC 2690
.::: 17CTT	2580 -TTGAAG; . ::: .CAGGAAG; 2550	2650 GAGA' :::: GAGA'	2720 GCTA ::::
2510 ACTCC(:::: ACTCT(25 TA-T : GACA	rcaa ::. :cag	CATAT:
.TGGG. :::: :TGGG. 2490	ACTGA .:::. GCTGT	340 TGTT: :::: TGCT(10 AATCZ : : : AAGCZ
500 2510 CCTATGGGACTCC ::::::::: CCTGTGGGACTCT 2490	570 TACAC::	2640 A-GTG:	2710 AACAA' :.:::
25 11 11 11 11 10 10	25 TCCI .: :	ACAC::: acaa o	TCTA:::
G-CCT::::GTCCT	.60 .accrgcrc .::::: .accrgrac 2530	30 AGAAA .:.: IGTAA	2700 AAACA ::.::
2490 2 ACAGCAGTCTG-CCTCC:::::::acc-cagrageTccTcc 2470 2480	2560 AGAC(: :: ATAC(0 SGACCCT-CCAGAAACA :::::::::::::::::::::::::::::::::::	690 2700 ATGAACACCAAACATC : .::: ::::: ACAAAC-CTAAGCATC 2660 26
2, CAGCA(: :: CC-CA(2470	25 ccccaG : ::: crccar	GACCCT : : : : : : : : : : : : : : : : : :) ::::: AAC-C' 2660
ACAG:: ACC-	ACCC: : GTCT	(V)	
Hum. Mur.	2560 2570 2580 2600 2610 Hum. ACCCCCAGACCTGCTCCTACACTGATA-TTGAAGAACCTGGAGGATCCTTCAGTTCTGGCCATTCCAG ::::::::::::::::::::::::::::::::::	2620 2630 Hum. GGACCCT-CCAGAAACA ::::::::::::::::::::::::::::::::	2690 2700 Hum. ATGAACACCCAAACATCT : .::: : ::::: Mur. ACAAAC-CTAAGCATCC 2660 267

Fig. 3R



• .				
2810 :TCCCTCCTGC :::: :: :-CCCTTGTGT	2880 :::::::::::::::::::::::::::::::::::	10 2950 11GAGCCTTCTTC 1::::::::::::::::::::::::::::::	3010 GGGATTCAGA	GGGATTCAGA 2990
2800 CAGGGATCTGCT .:: :: ATGGAGTTGGC- 2780	2870 GTCTGACCACCT ::::::::::::::::::::::::::::::::	0 2940 AGGGGTAATCTG .:: .:::: GGGCATAATCTG	3000 3010 TTCCTTTGTTTTGGGATTCAGA	CCTTTGTTTT 2980
2790 cccagg-grcargc ::::::: cccaagagrcrcra 60 2770	2850 2860 2870 AGGAAGTCTTTCCTGAAGTCTGACCACCTT .::::::::::::::::::::::::::::::::::	2930 GCAGAATGGCAG :::.:: GCTAGAATGGGG	2990 CCTCCCTTTT	CCTCCTC 2970
	Σ I Σ	2890 2940 2950 2950 2930 2940 2950 TTCAGTIGGGCAGACTCTGATCCCT——TCTGCCCTGGCAGAATGGCAGGGGTAATCTGAGCCTTCTTC ::::::::::::::::::::::::::::::	2960 2970 2980 2990 3000 3010 ACTCCTTTACCCTAGCTGACCCCTTCACCTCTCCCCCTCCCTTTCCTTT	ccttgrccagrgrgcrgaccc-rrgaccrcrrccrccrcccrrrgrrrrgggarrcaga 2930 2930 2940 2950 2950 2960
2770 2780 SACACCAACACTCCCTTCT- :::::::::::::::::::::::::::::	2840 CACCGCTGACTCC : .::.: CCATACTGTTT	2910 TGATCCCT: : :: : TTATTATTGTC	2970 2 GCTGACCCCTTC	CTGACCC-TTG 2950
2760 GCTGCCGCTTTGGA(:::::::::::: GCTGCTGCTTTGAA(2730 2740	2820 2830 TCCCTTACCAGTCGTGC ::::::::::::::::::::::::::::::::	2890 2900 TCAGTTGGGGCAGACTC :::::::::::::::::::::::::::::::::::	2960 CCTTTACCCTAG	GTCCAGTGTGG 2940
HumGCTG(:::: Mur. AGCAGCTG(2820 Hum. TTCCCTT ::::::: Mur. TTCCTTT	2890 Hum. TTCAGTTG :::::: Mur. TTCAGTTT 2860	29 Hum. ACTCCTT	MurCCTT 2930
_ ~	H 4	2	-14	-

Fig. 38

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	~		~		
3080	CTGTTTATTTTTTAAAAATATATAAGGCTTAAAAAAAAAA	•••	AGATATAA	3030	
3070	TTAAAAAAA		1 1		
3060	ATATAAGGC	••	A		
3050	TTTTATTAAA		AAACTGCTTGTCACAGACAATTTATTTTTTTAAAAA	3020	
3040	STTTATI	•••	ATTTATI	(*)	
3030		•	FCACAGACA	3010	3100
3020	AAACTGCTTGTCAGAGA		AAACTGCTTG1	3000	3090
V -7	Hum. A		Mur. A		(-)

Fig. 37

...::: Mur. GCTTTAAAG--

Hum. AAAAAAAGGGCGGCCGC



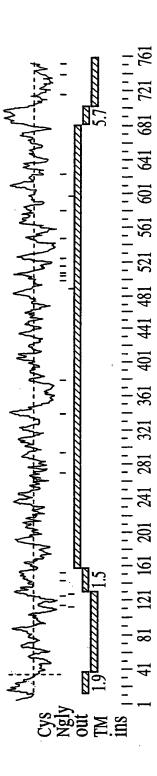


Fig. 3U



Ē 10 MAR 1 5 2004 FIRE TRADESORY

6 152 GCG Ø PCCT Q CAG R AGG 24 ATG $\mathbf{\Sigma}$ GCGAAGCGCCCTGCGACCCCGGCGTCCGGCGCGCGCTGGAGGACGCGAGGAGCC

26 212 C TGC CAT H K AAG K AAA 960 Ø GAA 떠 ACA ⊣ IGC ပ GAG ഥ $_{
m ITG}$ LCIC L CTG G GGG CIC ᅱ L CTG L CTG A GCG 929 Ø GTG > AAG ×

46 272 $^{\rm C}$ C TGC GAC Ω GAG ഥ Y TAC s TCC R CGC C TGC ATA Н TAT × TAT ⋈ TACC P CCA TAT L GGA ტ GAA 回 $^{\mathrm{F}}$ Y TAT W TGG

66 332 L CTT $^{
m F}$ $\overline{\mathtt{W}}$ F TTC Y $\overline{\mathtt{W}}$ Γ R AGG Q CAG I ATA S TCC LCIC A GCC R CGG GTG > $_{
m TGT}$ င TGC R AGG S TCC

9 99C

392 86 $^{
m Y}$ ATG Σ CGC 22 R AGG R CGG I ATC TIC 됴 $_{
m F}$ GGC ტ gcc Ø GGA C TGC င Tgc TIC 됴 CIT GTG > GGC G ATG Σ M ATG $_{
m L}$

106 452 N AAT P CCA CCC Q CAG R AGG T ACC TAC \succ TCC ഗ GTG \triangleright AAT Z TIC 됴 gcc Ø CCA Д GAG 田 GAG 団 ATC Н L CIG CCG വ CCG Д CCC

126 512 GGG G P GGA ᠐ GGA ტ CCA Д GAC Ω ACT Ещ TAC × \mathtt{TAT} ⊱⊣ CCC Д CCG بم GGG Ö CCG Д CAG Ø Q CAG A GCC GGA CCA Д CGC ᠐ P CC C

146 572 Q CAG PCCC S TCA AAC z PCCC P CCA GIC > CAG Ø TTC ഥ GCT Ø ATG Σ GCA Ø ATG Σ ICC വ AAT z GGG ტ GTC > PCCT AAC Z ATG Σ

Fig. 4A



GAA TAC C N T P TGC AAC ACG CCT A Y GCC TAC ' CCA CCCCCG CCC GTG AGT 9999

653 173

TAG A K GCC AAG K AAG Q V CAG GTA TGGGGTGCCCACGTGCAAGAGGAGAGAGAGAGGGGCCTTTCCCTGGCCTTTCTGTTCGTTGATGTTCACTTCCAG

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2549 2470 2628 2786 2707 2865 AACCTCCTGGGGAATTTTGTGGGAGACACTTGGGAACAAAAAAAGACACCCTGGGAATGCAGTTGCAAGCACAGATGCTG CCACCAGTGTCTCTGACCACCCTGGTGTGTGACTGCTGACTGCCAGCGTGGTACCTCCCATGCTGCTGCAGGCCTCCATCTAAA ATAGGCACCCAAAAGTCCGTGACTAAATTTCGTTTGTCTTTTTGATAGCAAATTATGTTAAGAGACAGTGATGGCTAGG SAACGCTGATCCTGCATATGGAAGTCCCACTTTGGTGACATTTCCTGGCCATTCTTGTTTCCATTGTGTGGTGGT IGAGACAACAAAGCACAATGTTCACTGTTTACAACCAAGACAACTGCGTGGGTCCAAACACTCCTCCTCCTCCAGGTCA PTTGTTTTGCATTTTTAATGTCTTTATTTTTTTGAAAAGCACACTAAGCTGCCCCTGGAATCGGGTGCAGCTGA TIGIGCCCACTICCIGGAGIGAGACAGCICCIGGIGIGIAGAAIICCCGGAGCGICCGIGGIICAGAGIAAACIIGAAG AAAAAAAAAGGGCGGCCGC

Fig. 4C

GCGGACTGGCCCTGAGCTGGCCGTACAGCCCGGCTTCGGACGGTCCTCGCTGGAGCC ATG GGC CGC

151

25 L L L G L L V E C T CTG CTG CTG CTG CTG CTG CTG CTA GTG GAG TGC ACT

Fig. 4D



AT BULL BY A

45 271	65 331	85 391	105 451	125 511	145 571	165 631	173 655
C TGC	F	M ATG	P CCA	P	P CCT	Y TAT	
D GAC	W TGG	R CGC	P CCA	G GGA	s TCA	CCC	
E GAA	F	R CGG	Q CAG	G GGA	N AAT	P	
Y TAT	Y TAT	R CGC	R AGG	P CCT	P	P CCA	
S	W TGG	I ATT	T ACC	D GAC	Q CAG	P CCT	
R CGT	L CTG	F	Y TAT	T ACC	V GTC	T ACG	
C H GC	R AGG	F	S	Y TAC	Q CAG	N AAC	
I ATA	Q CAG	G GGT	V GTG	Y TAT	F	ر TGC	
Y TAT	I ATA	A GCC	N AAT	P CCA	A GCT	Y TAC	
$^{ m Y}$	S TCC	G GGT	F	P	M ATG	S TCC	
T ACA	L	C TGT	T ACA	G GGA	A GCT	PCCT	
P	A GCC	C TGC	CCC	M ATG	M ATG	PCCT	
Y TAT	R AGG	FTTC	E GAG	O CAA	T ACC	PCCC	* TAG
L	V GTG	L CTG	E GAG	Q CAG	N AAT	P CCA	K AAG
G GGA	C TGT	V GTG	I ATT	A GCA	355 9	Y TAC	D GAC
E GAA	C TGC	G GGT	L	G GGA	V GTT	TACT	K AAG
F TTT	R AGG	M ATG	P CCA	P CCA	P CCT	T ACA	V GTG
Y TAT	S TCC	M ATG	P CCA	A GCT	N AAT	9 9	V GTG
W TGG	9 9	$_{ m CTG}$	P	P	M ATG	G GGA	Q CAG
C TGC	$^{ m C}_{ m TGT}$	$_{ m L}$	Y TAT	N AAT	9 666	H CAC	E GAA

CAAGATGCTACATCAAAGGCAAAGAGGATGGACAGGCCCTTTTGTTTACCTTCCCATCCTCACGATACTTGCTGATAG 734

Fig. 4E



1998 1682 1840 1919 2156 1603 1761 2077 2393 2472 2630 CAGATAAAGTGGTCAGGCTGAGATAAGACTCACATGATGCAGTAGTTGGCAGTGAACTTCGAAGAGACACTATCCACCA PCCCAGCCCATTCTCCTAATAGAAGCTGTGGGGCTGTTGTTGATGCTCTTTGGTCTCCACTCACATTTTGAAAATAG GGTGGTCCAAGGGAAAACTTGGATATTCTCAAAGCAAGCCCAGCTCTTTCAAGTCTTTTGTGGAGGACATTTGAATC SCTITCCTCTGCAGGAATAGGAAAGACCCAAGTACATATTTGCTTCCACTTAAAAATGAGGGTCAGAACCAGGCCTCAG TIGGACATCTATAGTTAAATAAAGGCCATTAGAGAGGGGAAATCTTTAAGTTAGGGGAAATTCTCTAAATGGAGACATT SCGTTTTATGAATCATCGTCTGGCTTTTTTTTAGTGCATGTATTGAAGTGAGGGTGTCCTTTGAGATCAGATGGGGAG AGTGAACTCTGCGGGGGGGGGGGGTGTCTCTACTCAGAGGGCTCCAACACCCTTTTCTTAGGTAGTTCTGGTGATGGGTT TTATGGGCACTATAGAGCTGAGGGGCACATTAGGCCGGGTAGTTACATTGACCCTTGGAGAGGAGGAGGACAGCCAAAG AAACTCAGCAAAGCAAGACCAGCATTGCTGAGTTAGAGCTAGGGTTGTATGTGATCCCAACAGAGATGTGCTGGCCTCA TGTAGTTAGAGATGCCATTTCCCCAGGTGAGAATCAGAGCTCATCCATAGATTTACAAGTAGTGGCTGGAGTTAACAGTA TGGAGTTCTTTTCCCTTGCGTAGTTAGTCACGTTGATGTGTATTTAAACCCAGGTTGAGACCTTGTGTACTAAGAGCAA SAGTATTCTTTACCACCTACAAGACCAGGAGGCATGGTGTCATTCTCCATTGGGGGTATTTATATGAGGTAGAGGTTCAG CAATGICTGTGTAAAGTTTTTGTTTGCCATTGAGCCCAATTGGAATTCCTTCTGACGTCAACACTGACAATGCCT PAAATGAGAAAATCAGAGCCATTTGATAAACTGTTACTTGTTGGATCAGGCATCCAAAAGTGTCTCTTGAGTGGACATT SAATCGACAGTAGCTGTGTGGGCTTAGTTTAAGGACTGAAAGCATÁGGGACTGGTAGACAGTTTCATAGGAAACTGCGG SGAAGGAATGGATACCTTTAAAGACAGTTTGTGGATGCAGATGCTGCCACCCATCATTGAGCACCCTTGTGTCTCTGGC CCTTTTTAAAATCAAGAAGCACAGTCAGAGCTGCCCCTGGGATTGCATCAGGGAACGGCTGATCAAGGCATTCAGTGTC ITCCTGTCACTGGATCCAGTACCCCTCCATGCTTGGGTCCTTGTTTTACATAAGACAACAAGCACAATGTCTGCTGTT ATGGAAATTGCACTTCTGGGTATATGTCCCAGCATCCTTGTTTTCTTATGTTTGGTGAGTAAGGCTCACCCCTTCCAGC <u> TACAATCAAGACGACTACATGGTCCAAACATTTCTTCTCTCTTCTATCACTTGTGGCTTTAACTTCCATTTCCTCCGTT</u> CATGACTAAATCTTATCTTTTGATAGCAAATCCTTTTAAGAAACTGAACAATTGCTAAGGCTCAGCAATTTTATACTC



化分分子

2788 2867 2915 AGCTCTACTTCTGTGTGCTGAGGTCCTGTAGAGCCGGGGCTTGGGCCACAGACATGAGGCAGACTTGTGCATGCTCTTTC TIGGCAACACTIGGCICATATITCTIGITCTCTTTTIGATAGAGICCTGTTTCCTATGTATTAAAAAATAATAAAGTG

Fig. 4G

	10	20	30	40	50	09	70
Hum.	Hum. MRRQPAKVAALLLGLLLECTEAKKHCWYFEGLYPTYYICRSYEDCCGSRCCVRALSIQRLWYFWFLLMMG	LLECTEAKKH	CWYFEGLYPT	YYICRSYED	CCGSRCCVRA	LSIQRLWYFWE	'LLMMG
		•••	•••	•••	•••		••
Mur.	Mur. MGRRLGRVAALLLGLLVECTEAKKHCWYFEGLYPTYYICRSYEDCCGSRCCVRALSIQRLWYFWFLLMMG	LVECTEAKKH	CWYFEGLYPT	YYICRSYED	CCGSRCCVRA	LSIQRLWYFWE	'LLMMG
	10	20	30	40	20	09	70
	80	06	100	110	120	130	140
Hum.	VLFCCGAGFFIRRRMYPPPLIEEPAFNVSYTRQPPNPGPGAQQPGPYYTDPGGPGMNPVGNSMAMAFQV	IYPPPLIEEPA	FNVSYTRQPPI	NPGPGAQQP	GPPYYTDPGG	PGMNPVGNSMA	MAFQV
		•••••••	••		••		•••
Mur.	VLFCCGAGFFIRRRMYPPPLIEEPTFNVSYTRQPPNPAPGAQQMGPPYYTDPGGPGMNPVGNTMAMAFQV	YPPPLIEEPT	FNVSYTROPPI	NPAPGAQQM	GPPYYTDPGG	PGMNPVGNTM?	MAFQV
	80	06	100	110	120	130	140
	150	160	170			-	
Hum.	PPNSPQGSVACPPPPAYCNTPPPPYEQVVKAK	AYCNTPPPPY	EQVVKAK				
			••		٠		
Mur.	Mur. QPNSPHGGTTYPPPPSYCNTPPPPYEQVVKDK	SYCNTPPPPY	EQVVKDK				
	150	160	170				

Fig. 4H

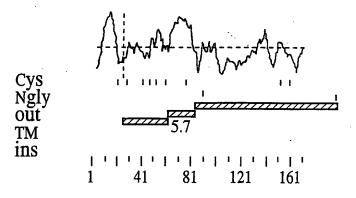


Fig. 4I

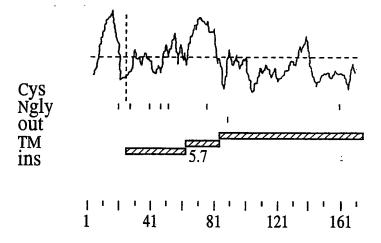


Fig. 4J



MAR 1 5 2004 LE

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GTCGACCCACGCGTCCGCAGCTTTGGACACTTCCTCTGCTTGAGGACACCTTGACTAACCTCCAAGGGCAACTAAAGGA

150 26 210 ATT Н ATC ACC Н ACA Q CAG AAG TCT വ TGT ACA S TCA വ ATG V GTC TCAAGAAAGGCCCAGCACAGCAGAAGATCAGCTGGATCTAGCTCCTGCAGGAG TAT LCTC N AAT WTGG L CTG L CTC \mathbf{F} $^{\mathrm{C}}$ G GGA W TGG CIC V GTC P CCA

46 270 GGA A GCT Q CAA V GTT GGT Y TAT D GAC LCIT A GCA R AGG Q CAG T ACT I ATT AGG 22 A GCA K AAG I ATC GGA ტ PCCT Y TAC

99 330 E GAG S TCT GGT S AGC L TTA D GAT PCCA L CTC K AAA K AAG E GAA K AAA $_{
m CTA}$ M ATG CAA E GAG I ATT ATG \mathbf{z} K AAG M ATG

86 390 S AGT ATC Н AAA × I ATA N AAT S TCA F TTT N AAT $^{
m Y}$ N AAC V GTA ${
m Y}$ D GAT V GTT K AAA L CTA F TTT E L CTT S TCT

106 450 L CTA GCG Ø AAA × I ATC GGA ტ V GTG GGA PCCT GIG **⇒** F TTT A GCT Γ TTG S TCA T ACC AAT z PCCA F TTT S TCA F TTT A GCC

126 510 GTT> TLL ᄺ LCIT CCA പ STCT E GAG $^{
m F}$. 666 WTGG GAC Ω T ACA S AGC I ATC N AAC A GCC T ACT 9 990 CAT 田 N AAC T ACC

ATG \mathbf{z} GAA 臼 AAT z \mathtt{TTA} Н AAC z AAG X L TTA ATT Н ည္သ വ AAA × GAG ഠ ATG Σ CCC GAG 団 A GCT F TTT S TCC AAC z Y TAT $_{
m CTG}$

Fig. 5A



166 630 186 690 206 750 226 810 266 930 30.6 1050 286 990 326 1110 E GAG E GAA $_{\rm L}$ G GG L Q CAA M ATG $_{
m L}$ L CTG P CCA N AAC M ATG A GCT S TCT F TTC T ACC TACC T ACA E GAA S TCT S TCC N AAC T ACA E GAA P FTTC S AGC S AGT L N AAC F TTC Q CAG Q CAA N AAT V GTT L CTC I ATC S AGC P CCA H CAT V GTT S TCC 9 9 9 9 T ACA N AAC L CTA YTAC R CGC A GCT $_{
m ITG}$ FTTT PCCA S TCC A GCC S TCC FTC E GAA F TTT H CAT I ATC Q CAA N AAC N AAT Y TAC V GTA S TCC N AAC P CCA Y TAC K AAG L CTA L CTA D GAT GGT LCIC A GCG S TCC I ATC N AAT PCCC A GCG L K AAG V . GTG S TCT I ATT E GAG I ATC CAA K AAA $_{
m L}$ Γ F TTT K AAA E GAG A GCA T ACC I ATA V GTC T ACT N AAC PCCT F TTT EGAA I ATT PCCC L E GAA $^{
m Y}$ $_{
m CTG}$ V GTT $_{
m TTC}$ TACC R CGG M ATG PCCT S AGT N AAC DGAC P CCA Y TAT S TCC E GAG M ATG S TCC A GCA D GAC LCTT S TCA E GAG L L I ATC T ACA I ATT A GCC I ATT Y TAC FTTC A GCC TACT V GTG S TCC K AAG I ATT N AAC P I ATC L N AAC M ATG A GCC IATC E GAG T ACC P GGA N AAT 9 9 9 9 PCCT Ĺ TTA TACT D GAC I ATT F TTC CIT R AGG I ATC I ATT T ACC V GTT Y TAC V GTG D GAC V GTT 9 960

74 / 95

Fig. 5B





446 1470 456 1500 346 366 426 1410 386 406 1230 1290 1350 AAC CCA TTC AGC TAT М ഗ \succ ATA S AGC R AGA L $_{
m L}$ K AAG Н CTG Q CAA R L CTG GTC TIC > 됴 Ы GGA AAT GAC AAC GGA AAA ტ ტ Ω Z X z $_{
m L}$ T ACC $\frac{L}{TTG}$ CC F TTT CAC വ 田 GAG S I ATT H CAC GGT CCA ഥ Д V GTT I ATT LCIT AAT CCÀ GAA Д Z 臼 W Γ L CCC $_{
m L}$ I ATT വ 990 A GCT S TCC Γ CIT GTA S TCG LCIT PCCT F TTC CAC GTT Ή S AGT R L CTA F TTT GGT F TTC TGA ACC E GAG F TTC I ATT G GGA S AGT PCCT S AGT R AGA N AAT Q CAA A GCC LCTT P CCA GCT N AAC E GAA Q CAG S TCA Q CAG V GTT Γ AAG F TTT $\frac{1}{1}$ E GAA GTT Q CÀG × GGG $^{
m F}$ S TCT R AGG K AAA I ATT K AAG G GAC $_{
m ITG}$ D GAT AGG $_{
m ITG}$ A GCA S TCA Ω 24 ATG TGG S TCC S TCC V GTC N AAT S TCA \geq TCC C TGC E GAG A GCC N AAT T ACA Q CAG GTT R AGA V GTC I ATT Γ V GTC E GAA

1579 1658 PTGCCGGTTTGCAATTCACCCCAGGAAGTAAATGGTCCTTAATCCTACAACTACTGTAAAACCCAGAAGGGGAAAGACAGT ITTGTTTGTTTGGGGCAAGAAGATTCTAGGACAAGAGCTAGGCATGTACTTCTGACCAGGTGGGTAAGCAACTCTAAG

Fig. 5C



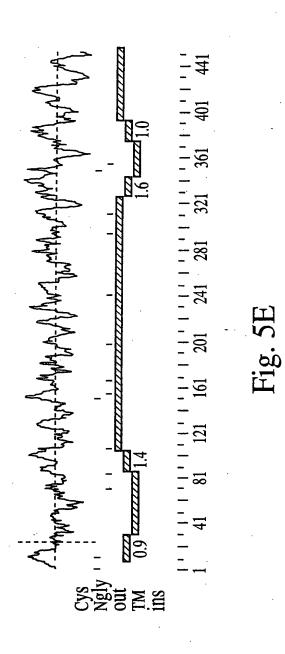
1980

TCTGTATTTGTATTGGTCATTCTCAGTGGAAATCCCTTAGGCCCTCTAGTGGTTTTCCCCTACCTGCATATTGGTTTTC 292299

Fig. 5T

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(A)	* TRADEMARKS

•			
10 20 30 40 50 60 MCTKT-IPVLWGCFL-LWNLYVSSSQTIYPGIKARITQRALDYGVQAGMKMIEQMLKEKKLPDLSGSESL : .: : : : : : : : : : : : : : : : : :	70 80 100 110 120 130 EFLKVDYVNYNFSNIKISAFSFPNTSLAFVPGVGIKALTNHGTANISTDWGFESPLFVLYNSFAEPME:.::.:.:.:.:.:.:.:.:.:.:.:.:	140 150 PILKN-LNEMLCPIIASE :: :: :: :: .: .: .: .: .: .: .: .: .: .	160 170 180 200 210 220 286 VKA-LNANLSTLEVLTKIDNYTLLDYSLISSPEITENYLDLNLKGVFYPLENLTDPPFSPVPFVLPERSN : :::::::::::::::::::::::::::::::::::
O 6 IEQMLKEKKI :: :. LQKELKRIKI 60	130 SPLFVLYNS:	140 LKN-LNEM: :.: .: SALRNKMNSQ:	210 IDPPESPVP . :::: NPPPEAPPVI
50 !: .:!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!!	120 STDWGFE: : : .	1, FHKKIESZ 190	FYPLENL:::
40 QRALDYGVÇ ::::.: QKGLDYASÇ 40	110 120 LTNHGTANISTDWGFESE :::::::::::::::::::::::::::::::	 SKVGWLIQI 180	200 YLDLNLKGVF :::: TLDVQMKGEF
30 40 <pre> <pre> <pre> <pre> <pre> </pre> <pre> </pre> <pre> <pre> <pre> <pre> <pre> <pre> <pre> <pre> </pre> <pre> <pre> <pre> <pre> <pre> <pre> </pre> <pre> <pre> <pre> <pre> <pre> <pre> <pre> <pre> <pre> </pre> <pre> <</pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre></pre>	100 EVPGVGIKA :::::: MVPNVGLKF 100	 NSVHVHISK 170	180 190 200 210 TLLDYSLISSPEITENYLDLNLKGVFYPLENLTDPPFSF
20 LYVSSSQTI IGTAVTAAV	90 100 SAFSFPNTSLAFVPGVGIK? .: .: .: .: :::: REFQLPSSQISMVPNVGLK!	TCSSCSSHI	180 NYTLLDYSL
SCEL-LWNL	SNIKISAE	KPI ::: :TSGKPTII	170 LEVLTKIDN ::::::
10 286 MCTKT-IPVLWGCFL- : . : BPI MARGPCNAPRWVSLMV	70 80 286 EFLKVDYVNYNFSNIK	286K : BPI SISADLKLGSNPTSGK 140 150	160 17 .LNANLSTLEVLT::::: .LQPYFQTLPVMT 220
286 MCTK : BPI MARG	70 286 EFLK BPI KIKH 70	286 BPI SISA 140	286 VKA- : . BPI VSSK 210

Fig. 5F

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290 RIMA : HVSA	360 ALPE .: ELKH	430 TSSK	
2 MVR DIH	3. 3. 3. 3. 3. 3. 3. 3.	(ETT)	
SQPEI NMKI(LNRFI : . : . LDRLJ 410	TDLK:	
) [LS(- NN 34	SLN SLN KLI	STI	
280 LIYI] KKFP	350 7CSL:	420 LLIS ::-	•
IAE .: IVAE)RLV ::: RLV	EGE 	
VLSF :- FLPE 330	LGQE		
270 NSQGLGNVLSRIAE1 :: :: :: TTKFFGTFLPEVAKP	0 330 340 350 36 NSTVETIVSMDFVASTSVGLVILGQRLVCSLSLNRFRLAL ::	410 NSDI : .	
SQGI TKFF	SVG	4 . : !. Y.	
FVQNS : :FRLTT	'VAS1 HTTC 390	HKFI ARVÇ 460	
FV SKFF	330 SMDFV 	400 LEPNPF ::::	**
260 SNH- ·· PKES	33 [VSN	4(PPLE	
SEIS.	TVETJ SLASI	LQQGI ::::: LQKGI 450	
LSTEE: LRDDM 310	NSTV SSI	AKLÇ .::3	
FAHFTAGVFNLTLSTEEISNH- ::::.::::::::::::::::::::::::::::::::	320 2PKN: :	80 420 400 410 420 ILHFGVLPLANAKLQQGFPLPNPHKFLFVNSDIEVLEGFLLISTDLK : :::::::::::::::::::::::::::::::::::	
2.5 3VFJ 5VLJ	MLT(AFA	VLP] ::: VLP	AP
FTA(: OEA(300	SIMM] DVQA] 370	HFGV] PILV]	3KS/
O FAHI LVY(310 DIPASIN TPAVDVÇ	380 SSIL!	450 QWR(
SAS SAS TAG	TLD	ILS	ISR
230 24 MLYIGIAEYFFKSAS : . : : :	300 PPIINLQPGNFTL :::: PPHLSVQPTGLTF 0 360	FENILS : .LQDIMN 430	LNL
AEY : SDY 2	300 NLQP(: SVQP'	370 EVLR: :	440 VWEG
230 IGI	3 IIN HLS	NIE PFP	4 FHV
MLY :.: MVY 0	300 310 320 330 340 350 360 TEPPIINLOPGNFTLDIPASIMMLTOPKNSTVETIVSMDFVASTSVGLVILGORLVCSLSLNRFRLALPE ::::::::.:::::::::::::::::::::::	370 380 400 410 420 430 snrsnievlreenilssilhfgvlplanakloogffplpnphkflfvnsdievlegfllistdlkyetssk::::::::	OPS
230 240 260 290 290 290 290 290 290 290 290 286 SMLYIGIAEYFFKSASFAHFTAGVFNLTLSTEEISNHFVQNSQGLGNVLSRIAEIYILSQPFMVRIMA ::::::::::::::::::::::::::::::::::::	300 310 320 330 340 350 360 286 TEPPIINLQPGNFTLDIPASIMMLTQPKNSTVETIVSMDFVASTSVGLVILGQRLVCSLSLNRFRLALPE .::::.:::::::::::::::::::::::::::::	6 H S · E 24.	440 286 QQPSFHVWEGLNLISRQWRGKSAP
28 BP	286 BPI	286 BPI	28

Fig. 5G

BPI

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09	286 MCTKTIPVLWGCFLLWNLYVSSSQTIYPGIKARITQRALDYGVQAGMKMIEQMLKEKKLPDLSGSESL	:	09	70 80 90 100 110 120 130 286 EFLKVDYVNYNFSNIKISAFSFPNTSLAFVPGVGIKALTNHGTANISTDWGFESPLFVLYNSFAEPME	: .: .:	130	150	IKN-INEMICPIIASE	•	KENP SISADLKLGSNPTSGKPTITCSSCSSHINSVHVHISKSKVGWLIQLFHKKIESALRNKMNSQVCEKVTNS 140 140 150 150 150	007	220	VKA-LNANLSTLEVLTKIDNYTLLDYSLISSPEITENYLDLNLKGVFYPLENLTDPPFSPVPFVLPERSN	•	KIDSVAGINYGLVAPPATTAETLDVQMKGEFYSENHHNPPPFAPPVMEFPAAHD	270
50	MKMIEOMLKE	: LLALQSELLR	50	120 DWGFESPLFV	: KWKAQKRFLK	120	140	TKN-	••	KKIESALRNK 100	O 6 7	210	PLENLTDPPF	•••••••••••••••••••••••••••••••••••••••	SENHHNPPFE	260
40	RALDYGVQAG	::. ::::	40	110 TNHGTANIST		110		 		KVGWLLQLFHI 100	O O T	200	LDLNLKGVFY		LDVQMKGEFY	250
30	YPGIKARITQ	:::: NPGLVARITD	30	100 FVPGVGIKAL	I SMVPNVGLKFS	100			3	NSVHVHLSKS.) -	190	ISSPEITENY	•	VAPPATTAET	240
20	KVSSSQT'I	.: TSTPEALGA	20	90 AFSFPNTSLA	: .:	06				TCSSCSBLI) -	180	NYTLLDYSL:	•	SVAGINYGEN	230
10 2	WGCFLLWNLY	.:: -PSILLALLI	10	80 YNFSNIKIS <i>P</i>	:::: YEFHSLNIHE	80		KPI-		SNFTSGKFT1 150	0	170	STLEVLTKI	•••••••••••••••••••••••••••••••••••••••	QTLPVMTKID	220
	MC'I'K'I'I PVL	: MGALARAL-		70 EFLKVDYVN	: RENP RIPHVGRGRYEFHSLN	70			() ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ; ;	SISADLKLG 140) r H	160	VKA-LNANL	•	>	210
C C	786	RENP		286	RENP			286		KEN T			286		RENP	

Fig. 5H



	230	240	250	260	270	280	290
286	286 SMLYIGIAEYFFKSASFAHFTAGVFNLTLSTEEISNHFVQNSQGLGNVLSRIAEIYILSQPFMVRIMA	SASFAHFTAG	VFNLTLSTE	EISNHFV	'QNSQGLGNVL	SRIAEIYILSQP	FMVRIMA
RENP	RENP RMVYLGLSDYFFNTA	::::::::::::::::::::::::::::::::::::::	:::: AGVLKMTLRDD	. : : DDMIPKESKFF		SLVYQEAGVLKMTLRDDMIPKESKFRLTTKFFGTFLPEVAKKFP-NMKIQIHVSA	:
	280 290		́ С	310	320	330 3	340
000	300 Suntanan	310	320	330	340	350	360
780	Z80 IEFFIINLQFGNFILDIFASIMMLIQFKNSIVETIVSMDFVASTSVGLVILGQKLVCSLSLNRFRLALPE	L LUL PAS LIMILITO	LTQPRNSTV	V T U SMOR V	NSTVETTVSMDFVASTSVGLVTL 	GORLVCSLSLNR ••••	FRLALPE
RENP	STPPHLSVQPTG	r FYPAVDVQAI	AVLPNSSL	ASLFLIGMH	TTGSMEVSAE	SNRLVGELKLDRLLLEL	 LLLELKH
	350 36	360	370	380	390	400 4	410
	370	380	390	400	410	420	430
286	286 SNRSNIEVLRFENILSSILHFGVLPLANAKLQQGFPLPNPHKFLFVNSDIEVLEGFLLISTDLKYETSSK	ILSSILHFGVI	PLANAKLO	QGFPLPNPH	KFLFVNSDIE	VLEGFLLISTDL	KYETSSK
RENP	SNIGPFPVELLODIMNYIVPIL, VI, PRVNFKI, OKGFPI, PTPARVOL, VNVVI, OPHONFI, FCA DVVVK	IMNYIVPIL'VI	TVPII.VI.PRVNFKI.OKGFPI.PTPARVOI.VNV	KGFPI,PFPA	RVOTANIVATO		: 7VK
	420 43	430 44	440	450	460	470 43	480
	440	450				-	
286	286 QQPSFHVWEGLNLISRQWRGKSAP	ISRQWRGKSAE					

Fig. 51

RENP

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	11	7]	4	٦	מ	ሩ	K	
ATTAGTTGTTACATTGGCAGGAAAAAATAAATGCAGATGTTGGACC	ATG	TTG	GAA	ACC	$_{ m TTG}$	TCA	AGA	CAG	` '

~	•	~~			<u> </u>	- ,			_				_
28	209	48	269	89	329	88	389	0	449	<	503	148	9
a	CAG	Z	AAT	ĿΪ	GAA	E	ACA	H	ATT	M	TGG	O	CAA
ഥ	TTC	Σ	ATG	H	ACT	×	AAG	M	$^{ m IGG}$	>	GTG	D	GAC
Σ	ATG	Ē	TTC	A	GCA	×	AAG	z	AAC	Ω	GAC	Н	ATA
X	TAT	A	GCA	>	GTC	Д	CCT	ഗ	AGC	Ēų	TTT	ഗ	TCC
Ø	GCG	ഥ	GAA	ഥ	GAA	Q	CAA	A	GCT	ტ	GGT	ы	CIC
\triangleright	GTG	Д	CCA	×	\mathtt{TAT}	>	\mathtt{GTG}	ტ	GGT	Ą	GCT	₽	ACA
ы	CIG	Ω	GAC	田	GAA	Ы	CTA	ტ	GGA	Ω	GAT	×	AAG
Н	ATT	>	GTG	[±]	GAG	ტ	GGC	>	GTT	A	GCA	н	CAC
П	CIG	Ø	GCT	ບ	\mathtt{IGT}	ሺ	CGA	Ή	CTA	Н	CTG	X	AAA
П	CII	×	AAA	വ	သည	Ъ	CCT	ტ	299	Н	ATT	ĸ	CGA
M	${ m TGG}$	⊱	ACT	X	TAT	Н	ATT	Н	CAT	Ĺτι	TTC	ഗ	ICI
Σ	ATG	Д	CCA	ტ	၁၅၅	ĸ	AGG	Ø	CAG	ტ	255	M	$^{ m TGG}$
딢	GAA	∇	ATG	Ø	CAA	Z	AAC	Ц	CIG	Ц	CTG	Ø	೧೧೮
Σ	ATG	H	CAT	Ħ	CAT	>	GTT	ı	TTA	Ŋ	AGC	Z	AAC
ፙ	AGA	>	GTA	Ø	CAA	ഗ	TCT	\triangleright	GTG	Z	AAT	ტ	GGA
Ħ	CAC	ഗ	TCA	Н	ATC	ı	CTT	>	GTG	Z	AAC	~	AGG
ഗ	TCA	z	AAT	Н	ATC	Н	ATC	Д	CCI	Д	သသ	ഗ	AGC
>	GTC	>	GTG	ഥ	GAA	> 1	TAT	ĸ	AGG	П	CTG	Z	AAC
н	ATT	Z	AAT	ഗ	AGT	ტ	GGG	Ø	ICC	Z	AAC	ტ	999
W	TGG	弘	AGA	Н	ATT	Q	GAT	ტ	GGT	ഗ	ICC	Σ	ATG

Fig. 6A



EMAS	%	ω	6
168	629	188	689
Н	ATA	ტ	GGC
>	GTG	O	CAG
P A	GCA	ഗ	TCA
Ч	CCT	×	TAT
П	CTT	ტ	GGC
Ω	GAC	>	GTC
ഥ	TTT	X	TAT
ĸ	AGG	X	TAT
M A	GCT	H	ATC
Σ	ATG	X	AAG
ഥ	GAG	Ħ	GAA
Ω	GAT	Ø	CAG
⅓	\mathtt{TAT}	ტ	CGC
ß	AGT	H	ACG
ĘЛ S	$_{ m TTC}$	×	AAA
Ø	GCT	Ø	CAG
ß	$^{ m LGG}$	н	TTG
F	TTC	Н	ATT
田	GAG	ഥ	TTT
Ω	GAT	Z	AAC

208	749	
Σ	ATG	
×	AAA	
H	ATC	
ĸ	AAA	
	CAG	
A	GCT	
Н	CIG	
迅	GAG	
വ	CCA	
Σ	ATG	
⊢	ACC	
ഗ	ICC	
দ	${ m TTT}$	
Ø	GCA	
Н	ATT	
ഥ	TTT	
ტ	299	
Σ	ATG	
⊟	ACC	
E	ACC	

228	808	
Ŀı	TTT	
×	AAA	
EI	G ACC	
ტ	GGG	
വ	သသ	
ഗ	AGC	
×	AAA	
Ø	GCA	
н	CAT	
×	AAG	
>	GTT	
₽	ACT	
Ø	သည	
H	ATA	
വ	သည	
Ø	GCA	
ப	TTA	
Ø	GCT	
ĪΞ-I	TTT	
×	TAT	

83	/ ₋ 95	erinaa erasiins
248	869	268
O	CAG	I ATT
×	CTG TAT CAG	Q CAG
	CTG	D GAT
ഥ	TTT	L
ഥ	GAA	I ATT
×	AAA	V GTG
F G K K E	AAA	Q CAG
ტ	299	255 GGC
됴	$_{ m LLL}$	C HGT
Н	${ m TTG}$	CII
ტ	GGA	Y TAC
K G L	AAG	I ATT
	ATC	V GTT
Σ	ATG	L
Σ	ATG	Q CAA
Ω	GAT	R AGA
Д	CCA	L
L L L P D M M I	CIG	F
ы	${ m TTG}$	R AGA
П	$_{ m TTG}$	T ACC

268	929
Н	ATT
Ø	r n
Ω	GAT
ы	CTT
Н	A;
>	GTG
Ø	CAG
ტ	CCC
ບ	TGT
ы	CTT
X	TAC
Н	ATT
>	\mathtt{GTL}
Н	CTT
Q	CAA
K	AGA
П	CIC
ഥ	TTT
ጸ	AGA
₽	ACC

288	686
ĸ	CGA
ഗ	AGC
Σ	ATG
z	AAC
Σ	ATG
Z	AAT
Z	AAC
₽	ACC
z	AAC
ഥ	$_{ m TIC}$
ტ	GGA
ტ	GGT
П	CTG
니	CTT
П	\mathtt{TTA}
Σ	ATG
Н	ATC
Z	AAT
ഗ	AGT
ပ	\mathtt{TGT}

³⁰⁸ W TGG H CAC N AAT T ACA A GCT S AGT A GCA

328	1109
z	AAT
×	AAA
H	ACC
囝	GAG
വ	AGT
ტ	999
Z	$^{\mathrm{IGG}}$
Ω	GAC
Ēų	TTT
¥	GCA
ፚ	CGG
Ы	CIC
闰	GAA
ŋ	GGT
ഗ	\mathtt{TCI}
z	AAT
>	GTG
Ą	GCA
	CAG
ഗ	AGC

408 388 424 1397 D GAT Γ Q CAG V GTC M ATG V GTG M ATG K AAA T ACG H CAC $_{
m L}$ M ATG A GCT V GTG H CAT GAT I ATC D GAC \overline{W} * TGA I ATC $_{
m L}$ E GAA R AGA E GAA V GTA V GTC E GAA PCCT P CCA I ATT N AAT A GCC R AGA N AAT E GAG $^{
m Y}$ N AAT $^{
m Y}$ S TCA $^{
m C}$ K AAG M ATG R AGG LCTT CGG H CAT V GTA W TGG R CGT $^{
m Y}$ D GAC H CAC S Q G TCC CAG GGA P CCT I ATC T ACT P CCT Q CAG LCTC P CCA GGT A GCT L Q CAG N AAC G GGA D GAT T ACC E T N GAG ACC AAC N AAT T ACA $\frac{L}{TTG}$ V GTG C TGC TGG G GGT 3 E GAG AAA ATG WI ATC CAG GAG GCA S TCT 口 ACA L O

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TRADEMARY

1476 1634 1713 2029 1792 1871 1950 AGCATCTGACACTGACGATCTTAGGACAACCTCCTGAGGGATGGGGCTAGGACCCCATGAAGGCAGAATTACGGAGGAGCA ATTTTGGAGCACTAAAGTAAAATGGCAAATTGGGACAGATATTGAGGTCTGGAGTCTGTGGATTATTGTTGACTTTGA **LTAAAGTACTTATTAGGTAAATAGAGGTTTTTGTATGCTATTATATATTCTACCATCTTGAAGGGTAGGTTTTACCTGAT** CAAAATAAGCTAGACATTTTCACCTTGTTGCCACAGAGACATAACACTACCTCAGGAAGCTGAGCTGCTTTAAGGACAA CAACAACAAAATCAGTGTTACAGTATGGATGAAATCTATGTTAAGCATTCTCAGAATAAGGCCAAGTTTTATAGTTGCA

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Fig. 6D

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Fig. 6E



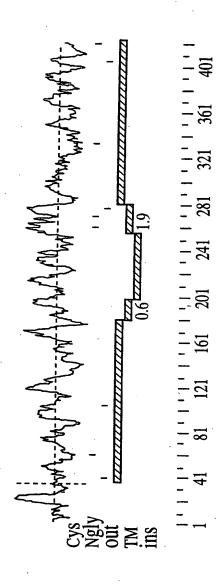


Fig. 6F

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1	PRADEMARKS PARADEMARKS

10 20 30 40 50 60 294 MLETLSRQWIVSHRMEMWLLILVAYMFQRNVNSVHMPTKAVDPEAFMNISEIIQHQGYPCEEYEVATE : :::::::::::::::::::::::::::::::::::	90 100 110 130 PKKTGSRPVVLLQHGLVGGASNWISNLPNNSLGFILADAGFDVWMGNSRGNAWS :::::::::::::::::::::::::::::::::::	160 170 180 200 SYDEMARFDLPAVINFILQKTGQEKIYYVGYSQGTTMGFIAFSTMPELAQKIKM :::::::::::::::::::::::::::::::::::	210 220 230 240 250 260 270 294 YFALAPIATVKHAKSPGTKFLLLPDMMIKGLFGKKEFLYQTRFLRQLVIYLCGQVILDQICSNIMLLLGG ::::::::::::::::::::::::::::::::
40 50 AVDPEAFMNISEIIQHQ ::::::::::::::::::::::::::::::::::	120 NSLGFILADAG.:::::::::::::::::::::::::::::::::::	190 3YSQGTTMGFI : :::::::: 3HSQGTTIGFI 180	260 2LVIYLCGQVI : .:.: **********************************
40 MPTKAVDP : ::: SGGKLTAVDP!	110 ASNWISNLPN .:::. SSNWVTNLAN	180 KTGQEKIYYVC :::::::::::::::::::::::::::::::::::	250 EFLYQTRFLR(:::::::: EFLPQSAFLKV
30 MFQRNVNSVH 	100 VLLQHGLVGG :.:::: VFLQHGLLAD	170 LPAVINFILQ: ::: ::::. LPASINFILN: 160	240 MMIKGLFGKKI .::::::
20 30 MEMWLLILVAYMFQRNVNSV ::: -KMRFLGLVVCLVLWPLHSE			230 SPGTKFLLLPC :: .:. ::: SPMAKLGRLPD
10 LSRQWIVSHR	70 80 DGYILSVNRIPRGLVQ ::::: .::: . DGYILCLNRIPHGRKN 60 70	140 150 294 RKHKTLSIDQDEFWAF :::::::::::::::::::::::::::::::::::	210 220 294 YFALAPIATVKHAKSP .::.:.:::::::::::::::::::::::::::::::
294 MLET : LAL M	70 294 DGYI :::: LAL DGYI 60	140 294 RKHK' :::: LAL RKHK' 130	210 294 YFAL. ::: LAL FFAL(

Fig. 6G

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Fig. 6H

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75	22 135	42 195	62 255	82 315	102 375	122 435	142 495	162 555
GCT	T ACC	L	F	S AGC	Q CAG	E GAG	C TGT	T ACT
ATG G	D GAC	I ATC	$_{ m L}$	V GTC	L CTG	N AAT	E GAG	F TTC
AG A	M ATG	V GTC	S AGC	Q CAG	GGG	$_{ m L}$	E GAG	K AAG
ACCA	P	IATC	T ACC	9 9	I ATT	Q CAG	A GCT	E GAG
CCIC	F	F TTC	V GTG	V GTG	D GAT	Q CAG	Y TAT	A GCT
CCCGGGGCGCAGCATTGCCCCCCCTGCACCACCTCACCAAG	TACC	T ACG	V GTG	S TCT	A GCT	V GTG	NAAAC	$_{ m L}$
CTGC	P CCA	A GCC	CGG	W	S AGC	P	E GAG	Y TAC
ממממ	K AAG	L	L	E GAG	I ATC	T ACC	G	$rac{ ext{L}}{ ext{TTG}}$
IGCC	P	A GCA	L	S TCT	W TGG	ر 999	$_{ m L}$	V GTG
GCAT	9 9	T ACT	W	S AGT	E GAG	T ACA	R	P
CGCA	A GCT	L	FTTC	F	S	L	W	D GAC
9999	Y TAT	TTT.	L	N AAT	S AGT	T ACA	T ACC	P CCA
JCCC	F	I ATC	R AGG	V GTG	F	I ATC	F	L
2999	P	M ATG	TACG	A GCT	A GCC	N AAC	E GAG	GGG
GCGA	F	I ATC	K AAG	L	K AAG	V GTC	E GAG	K AAG
CACG	T ACA	IATC	G GGA	I ATC	$^{ m Y}$	G GGA	N AAC	E GAG
CGIC	H CAC	S AGC	R CGG	A GCA	S TCA	G GGT	$^{ m Y}$	L CTG
CACG	G GGA	A GCC	I ATT	A GCT	TACA	$_{ m L}$	N AAT	A GCT
GTCGACCCACGCGTCCACGGCGAGGGCT	L TTG	$_{ m L}$	9 9	999	N AAC	9	I ATC	K AAG
GTC	T ACT	TACT	PCCT	I ATC	TACC	V GTC	TACC	A GCA



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242 795 262 855 282 915 202 675 222 735 302 975 322 1035 342 1095 V GTG V GTG S TCA L VGTG F TTC L A GCT S TCA PCCT L CTG S TCT $_{\rm TGT}$ A GCT GGA $_{
m L}$ $^{\rm C}$ T ACC M ATG A GCT A GCT L CTG K AAG GGT D GAT P Y TAC S TCC $\frac{L}{TTG}$ $_{
m CTG}$ $_{
m L}$ G GGC I ATT E GÀÀ PCCT H CAC L L CTG $_{
m L}$ GGA R AGG E GAG D GAC D GAT GGA M ATG Q CAG H CAC T ACA H CAC Q CAG P CCT K AAA A GCG V GTG FTTC L CTG TACC P CCT S TCC PCCC S AGT L CTG I ATC P $_{
m ITG}$ Q CAG N AAT W TGG K AAG H CAC R CGC A GCC 9 9 $_{\rm TGT}^{\rm C}$ T ACA M ATG E GAG P A GCA Y TAC L T ACG PCCC I ATC R AGG L CTG E GAG S AGT Q CAG L A GCC S TCA \overline{W} H CAC M ATG D GAC K AAG R CGC $\frac{1}{1}$ TACC \overline{W} $_{
m TTC}$ A GCC PCCC A GCT C TGT L CTC $^{
m Y}$ သ TGC L CTA A GCC V GTG M ATG D GAC $^{
m Y}$ M ATG L CTA L A GCG S TCA PCCT S TCC A GCA E GAA 999 FTIC Y TAC T ACA G GGG M ATG D GAT R K AAG C9 A GCC A GCA V GTG H CAT A GCT YTAC TACC P V GTG M ATG H CAC $_{\rm L}$ GGT S AGT R CGC S TCC S AGC WTGG S TCC Q CAG Y TAT T ACT . b P S TCC R AGA L CTA V GTA \mathbf{F} TTC H CAT $_{
m L}$ N AAC S AGC A GCT MATG L CTG \mathbf{F} TTC L CTG $_{
m L}$ F TTC L CTG E GAG

Fig. 7B



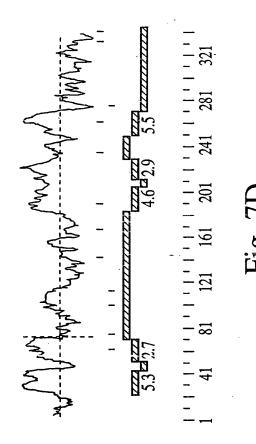


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496 2049 1970 1891 CATICCICCCCGIGGAGGCCACCIGGACIICCAGICIGGCICCAAACCICAIIGGCGCCCCAIAAAACCAGCAGAACIG AAAAAACAAAACAAAAACAAAAAGCCCTAAGGGACTGAAGAGATGCTGGGCCTGTCCATAAAGCCTGTTGCCATGATAAG SCCAAGCAGGGGCTAGCTTATCTGCACAGCAACCCAGCCTTTCCGTGCTGCCTTGCCTCTTCAAGATGCTATTCACTGA AACCTAACTTCACCCCCATAACACCCAGCAGGGTGGGGGTTACATATGATTCTCCTATGGTTTCCTCTCATCCTCGGCA CCTCTTGTTTTCCTTTTTCCTGGGTTCCTTTTGTTCTTCCTTTACTTCTCCAGCTTGTGTGGGCCTTTTGGTACAATGAA AGACAGCACTGGAAAGGAGGGGAAACCAAACTTCTCATCCTAGGTCTAACATTAACCAACTATGCCACATTCTCTTTGA SCTTCAGTTCCCAAATTTGCTACATAAGATTGCAAGACTTGCCAAGAATCTTGGGATTTATCTTTGTATGCCTTGCTGA CACCTACCTTGGCCCTCAAACACCCTCACAAGAAGCCAGGTGGGAAGTTAGGGAATCAACTCCAAAACGCTATTCCT CGTCCCCTGGGGTGGTTCAGAAAGATGCTAGCTCTGGTAGGGTCCCTCCGGCCTCACTAGAGGGGCGCCCTATTACTC | IGGAGTCGACGCAGAGAATCAGGTTTCACAGCACTGCGGAGAGTGTACTAGGCTGTCTCCAGCCCAGCGAAGCTCATGA CCCTCAGGGTGGCTGTTACCAGACACCCAGCACCAATCTACAGACGGAGTAGAAAAAAAGGAGGCTCTATATACTGATGTT

Fig. 7(





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PRADEMARKS TRADEMARKS	

30 40 50 60 70 30 11 SIIMIFLTALATFIVILPGIRGKTRLFWLLRVVTSLFIGAAILAV 1:	30 PTW	FDI	200 ILSM	LFL	CVL::::260
60. VVTSLFIGAAIL. : .: YVLMLAVGGALI.	50 130 -YNEEF	::: YNEG 0	NV - №	VVILIN O	260 ITLTTGLLCVI ::::: LIFAIGILCVI 260
) SLFI : .	5 N-	: ELYYI 120	'LLA	: CLSV 190	TLT
60 STVV SYVLM	NET1	 SDMT	190 FLCW	FACW	260 WITLTTGLLCVL :::: FCFYLIFAIGILCVL 250
WLLR ITVT	40 50 120 130 TGTPVQQLNETINYNEEFTW	SSNDVLPGSDMTELY	WVA	AIWEA 180) \
50 TRLFT :. KRVV	, GTP	SNDV	SAMI	HAA] 18	250 HGPAF : LTATF
RGKI:	[RLLS	180 3HYT	 TYHE	LHTHH ERVDL
30 40 50 IMIFLTALATFIVILPGIRGKTRL:: .: .:	30 L		140 150 160 170 180 200 RLGENYAEECAKALEKGLPDPVLYLAEKFT-PRSPCGLYRQYRLAGHYTSAMLWVAFLCWLLANV-MLSM	SGISSMAEALHHGLENGLPYPMLSVLEYFSLNQDSFDWGRHYRVAGHYTHAAIWFAFACWCLSVVLMLFL 130 140 150 160 170 180	210 220 260 260 260 260 250 250 260 260 260 260 260 260 260 260 260 26
40 IVII ILII	110 VNITI	: · · : NVTI	O YRQY	GRHY	240 .LGA. . :. .IAFTGE! 230
LATF : LIAY	1 LGGV	: : !QKV	170	SFDW	PLHL:
LTA	20 20 20	 ÆIG] 90	PRSI	.NQDS1 160	O LTSPCPLHL: ::: LLSPCELRI
30 IMIE FSVE	20 30 90 100 110 YKAFSSEWISADIGLQVGLGGVNITL-	FRGHSNERILAKIGVEIGLQKVNVTL 80 90 1	O KFT-	YFSL	230 TSLT : LL
LASI. :: SI]	VISA	XILA O	160 /LAEK	VLE.	SMA
IDTT1	SSEV	SNER 80	50 160 GLPDPVLYLAEKFT	PMLS'	LLFE : . CLVY
20 TFPM 	90 YKAF	FRGH	50 GLPD	SLPY	220 DLLALL ::::
YAGPKPTFPI :	10 INTS	: IYTQ 70	ALEK(LEN(GIF(:: GIS(210
10 PFYAC :AS	80 GQVS1	SQM.	CAKA.	LHHGL 140	O LLATC
HTFP : :	8 VSVG	: NASG	140 YAEEC	1AEA	210 3GYML.
MATLGHT : .: M-RIAH-	SSEI	YPCV 60	GEN	GISSN 130	VLVYC .: HNAYF 200
10 20 30 40 50 60 70 20 30 20 50 60 70 296 MATLGHTFPFYAGPKPTFPMDTTLASIIMIFLTALATFIVILPGIRGKTRLFWLLRVVTSLFIGAAILAV :	10 80 296 NFSSEWSVGQVSTNTS		6 RL	P SG	210 220 230 240 250 250 250 250 250 250 250 250 250 25
296 CRP	29.	CRP	296	CRP	296 CRP

Fig. 7E

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(F	TATE TRADEMET

270 280 320 296 LGLAMAVAHRMQPHRLKAFFNQSVDEDPMLEWSPEEGGLLSPRYRSMADSPKSQDIPLSEAS	CRP CGLGLGICEHWRIYTLSTFLDASLDEHVGPKWKKLPTGGPALQGVQIGAYGTNTTNSSRDKNDISSDKTA	270 280 290 300 310 320 330	330	296 STKAYCKEAHPKDPDCAL		CRP GSSGFQSRTSTCQSSASSASLRSQSSIETVHDEAELERTHVHFLQEPCSSSST	340 350 360 370 380	Fig. 7F	
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